SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						*NPGLSW*TDFKCLI
3157	8654	A	3417	3	796	PGPRAPPIRCSPLRSAPRRPST*SAA AWPASAAAGFCPCFYSAPSPSTSSR WPAAAGCSLATTAKTSSRVVEMLP RRAAAAGSYEGRAVRA/VMEYAW GRAAA/DHALSVASSILVILFHPLLL RPLCWTPECLSS*EVIGGLLALAAV FQIISLGNLPREVHPDLHPSCQAPLS LTSITGAYGFGVGQPRIILTRLCLLL LAASPTTEDGPSGAMPSPGTSTHLP NLGMKCGRKSLPAEMGLPEGRKLF LPGGLWNPIFWPVFHHY
3158	8655	A	3418	2	603	GFFFFKIVLIQDLFPSTPLPSSVHSGD YGDSGQDPSGTRNTFRRFCSPSFPPS CQLPRPEAHTHANTRNPPPSPHLLSF PHQSSEP*EGVKSLFEEA*KWGEMA ITP*PTPLWR*LWRTPNSFPLSGQPF STP\RPSVPSPIQPKTKHVQQHPPPAS T*KTGSVPTSLTPSTGVLGEWPPEDP AKGLMPEGKEEQKAFGP
3159	8656	B	3419	34	375	MLLGRLTSQLLRAVPWASLPRKGA QLELEEMLVPRKMSVSPLESWLTA RCFLPRLDTGTAGTVAPPQSYQCPP SQIGEGAEQGDEGVADAPQIQCKN VLKIRRRKMNHHKYRKL*
3160	8657	A	3420	2	361	YSTSPAGQVGRLSPSQGGPAGAGG DAG/TPGRCPSAPWRAGSRPAASCP DWIPG/PAGHVAPPQSYQCPPSQIGE GPGGTPETQADQVRERPEAHLAEG GAKGSPRRAGRPPRSTCGANESG
3161	8658	A	3421	1	417	RITAATGGKGGARLICPAGR/CLGV CQPSGASFSPAFSQMPSSPCSAPSPI WLGGHW*DCGGAT/CPCGPGIQSG QEAAGREP/GSPGG*RTSSWGPASPP APAGPPCEGERPPYLGRPAMCCKG ARRPGCPALQRRAKAGGR
3162	8659	A	3422	31	756	GRRALRQAGPGSSREGPGARQRDS RGGEPGEGAGLPVLGPFGASERDTA RVGGLGASGRELCWKQSPPCGLGW RREKGSEGRGGTRRPSPGPPATTEG AAA*PE/PGTCVPAPLGP\GPPPTDH APGAPDFPAVEGRSLGRRPPALAQS /P/GSAGQPGLRSPFTAH/QPAGPGRR GLSPSQGGPAGAGGDAGPQEDVRQ PPGELGSRPARFLPQTGLPGPAGTC GLHRNPTQCPPSPDRGKGPKQGG
3163	8660	A	3423	69	258	PRTNRCATNHTPANF*FFVETGFLH VAQAGLELLGSSSSPALAPKQLVTG ASHHTRPQ*NFLQ
3164	8661	A	3424	8	292	QSFLFLKTRYLLRHP\GWNTVAQ*Q LTVVTSRLN*SFHLSLPSS\WAIAVR MPPCPANFLFF/TRDRVSLC*PRLVS NTWVQMILLPQPPEMLGLQA
3165	8662	A	3425	123	357	WGKRPGQGGRNPWGPPLPGGK/PP KKGFLGPFPTGRFQGSSPGL*KGPFL KGGP/QF*KPKPGSQNRVFKPPKIWE TPLGN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3166	8663	A	3426	2	311	FHSCYPGWSAMVRSQLTATSASQF K*FSCLS/LPSSWDYKCAPPHPANFL FLVEMRFHHVLVRLVLNS*TQVIHL PRPPKVLGITGVRLGAQPCTFFFFYC SSV
3167	8664	A	3427	7	534	TSDFIYKALKLQQEVPKAKSHLVQN YRFFFFFFLRWSLAPVAQTGVQWH DLSSLQPPPPGFKRFFCLSLPSSWDY RCPPPRPANF*FLVETGFHHVDQAG LKHLTSDDPPASASPSAGITGVHPRP GQENQDLPGLCVDQLYTENSRFFSK NYYQTPNFTSRKRDLKISVFFFPA
3168	8665	A	3428	368	688	LTVEFLNLLNILSLVCFIHQTN*IICY FNT/SSSHQNAYI*EPHVPS*GQRGK ASRQRG*TPPRSGTAASWPRVEK*R EARPQNPAQQTTYVRESPTDASPSS PKMAA
3169	8666	A	3429	1	90	FFFVLSHQRNLCLRRYSRDMAAIIK SKFFL\WPGRVAYAYNPSTLGGRGG QIT*AQEFKCS*AAIIKSKFFL
3170	8667	A	3430	259	331	RNE*LLTRFSPLSLSH*VLGVSMF
3171	8668	A	3431	1	639	LGKFHTFQMSPGGGVGLLSL*SYRN SCLAG/GGCDHMSVHVCIRARGVK VRSKNSNHPTETRK\VLGGMRLSLT RESSISDSMWLARKQTLHTPVMMQ TPHLTPTI*EEPQRI\RPE\DTFMSV/Y YPMQTEHHQTPLDYNRRGTSLLED DEEPIVEDVMMSSEG\RIEDLNEGM DFDTMDIDLPPSKNR\RERTE\LKAD FFDP\ASIMDESVLG\VSMF
3172	8669	A	3432	1	354	LETSPLMFTMLDRDMSG/TMGFNEF KELWAVLNGWRQHLSSFDTDRSGT VDPQELQKALTTMGFRLSPQAVNSI AKRYSTNGKITFDDYIACCVKLRAL TDSFRRRDTAQQ\FIQCVMSV
3173	8670	A	3433	1	788	MAYPGHPGAGGGYYPGGPSVVKEE NLIRQNDVYVFPVSQYGGAPGGPA FPGQTQESL\YGYFAAVAGQDGQID ADELQRCLTQSG\IAG\GYKPFNL\ET CRLMVSML\DRDMSGTMGFSIEF\K ELLGLLLEWAGR\QHFISF\STDREW EQ*DPQELPEGP*QTMGF*V*VPPGC *ISFAKRYST\NGK\ITFDDYIACCVQ T*GVFTDSFSKTGILAQQGCLLNFPI WIDFHFNCVHGVFKSLGSCMNVIN DSNWSSPLLVLFAFG
3174	8671	A	3434	6222	7046	RTVTTFLSKDSHGVYCAQGGKIPDH QNPQCNRKQHPVSTILMLDKASFC QLRKRKHNLSVNCINRNPFMSLKN TSWHSSLSVTQRHQQSKLHFQGSI LLH*PSQNIL/SNI*KCINYC*HCSSV LLSYLFIETESYSVAQAGVQWHDLG LLQLLPLRFKQFSCFSLPSSWDYRS APSCPANFCILVEMGFCHVGQAGL KLLASSDPPALASQSAGITGVSHYT QPCSPFLKSTGLFSCKVLSNPYHKG RIYLGRMCFLNSTWHLVKSTLFCPL FI

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3175	8672	A	3435	3	287	SRSVAQAGVRWRDLSSLQPPPPRFK QFSCLNFPSSWDYRCAPPRPANF*I LAEMRFRHVGQVGLELLTSGDPPA SASQSAGITDTSHCAWPFTF
3176	8673	C	3436	88	303	MTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPEVLECLSTQQVKSL QTLGGAAVSHKTNICLPFTKLW*
3177	8674	C	3437	354	416	MKESPGGELPQTGKKPVFLF*
3178	8675	A	3438	274	460	TLKNLRSAASLTLGNPASPAHSSILS CPMRGHCRTL*KCHDWSFRAKMPS PFPQVGIYPPPN
3179	8676	A	3439	480	613	LSFRAKMPSPFPQVGIYPPPN*GPIC LLCFSFLCECVFYRNHLD
3180	8677	A	3440	1	864	YPTTPYQHHPISSPPPIPTHNHHQKP PTPSHRPQPTQRYTYHHNHTALTPI APTRQSNPPHNTHHHTPS/TPRTNSS PPH\HHTLPQRIPPYPPGT*HTPQAHS HPAG*RASSQPRRAPSPASRPSPTDP ALRANPLSRSYGSGLPTFPYLHCSN MPKACSPWRPAADMCTAR\PRFRPF KPDFQGPARAHRTPPETRRFPRHGPI SRGEPI\PGQPCPSQRKENSTPEFPPA SSGIGRVTDTGRLAAAPSPPLRIRGS EPDSPFESAEGHRRPSPRPFRTALAQ SLRNE
3181	8678	A	3441	23	266	EMESHSVT\RLECSGAISAHCTLRLP GSSDSPASAS*EAGITGMCTT/ARLIF GFHHVGQAGLKLL/NIVILLPRPPKV LGLQA
3182	8679	A	3442	840	887	
3183	8680	A	3443	127	593	DKATKLTKFRSYAAVILKIHFVLTW VILFRRKIIRDETLKLLDLISLSVGKG QCYRVVFFWFFFFFFEMKSHSV\TR LECSGAISAHCNLCLPGSSDSPASAS LVAGVTGM*HHTQPIFVFLVATGFH HVGQGWSRTPDIRVIRPPWPPKVLG LQA
3184	8681	A	3444	2	514	FFFFFLRQSL/DSVAHTGGQ/WGGS/ LQPPPPRFEGFLGLKLLGS*HYK/PP RMANFIFSRDGVFAMLARLVLNSS ASSDLPGLASHSAGITG\VSHHARPI FSYKEHQSY\GLRACPAPV*PHLSYL QPQPQYFQIRSHTEAPGST/WNFGE DTIQPSTFSFYLT*KIIPILYRVKK
3185	8682	A	3445	2	147	FFFCRD/RSLTMLPRLVLYSWAQVIL PSWPPKMLG*QAQATVPSPPKSIN
3186	8683	A	3446	2	328	TITYRGAKIRITSDSSSETMQAREE* SEIF*VLK/ESSSPH*PKILYSGKLSFK SKGEIK/YF*GKQN/LKEFVSSRPVL QGMLKVVLQREGKLYRSETQTYKK KEKASEKE
3187	8684	A	3447	1	357	GDRVLLCCPG*SADHSSLQS*PSGL KRYFCLGLLSNWKHRCMPPCPANF FNFYFCRDK/SLPMLPRLVSNSW\AQ GIFLSQPPVSVGDYRCGAYHALTLFI YGRMGVFAMLAQAGPQTPGL
3188	8685	A	3448	2	84	GLTLLPRLVSNSWPQEILLPW/PPKV

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						LKL*AQAGLKLLASGNPPALAPKVL KL
3189	8686	A	3449	1	439	
3190	8687	A	3450	1	552	GNEFSILKSPGSVVFRNGNWPIPGER IPDVAALSMGFSVKEDLSWPGL\AV GNLFHRPRGYPSWVM\VKGSGTKL ALTPQAVVISYP\LENRVYMVGKAN SVF\EDLSVTLRQLRNRLFQENSVLS SLPLNSLSRNNEVDLLFLSELQVLH DISSLLSRHKHLAKDHSPDLYSLEL AGLDEIGKRY
3191	8688	A	3451	3	1111	ILKSP\GSVVFRNG\NWPIPRE\RDPP DVAA\LSHGLPL*KKDLSWPGLAVG NLFHRPRAT\VMVNVNGVNKLDLP P\GSGIS\YPLENAVPFSLDSVANS\IH SLF\SEET\PVVLQLAPSEERVYM/VK GRANSVFEDLS\VTLRHSRNRLVFK KTLFLSFTPPQILLSRNNEVDLLFLS ELQV\LHDISSLPSRPKHL\ARDHSPD LYFTGSWAGL\DEIG\KALLGEDSEQ FRDASKILVD\ALQKFADDHVPVFM VGNPVVELVHCPSHLNTSPPLGKTR DLPLRPKQAQEPQQVPYNLA\YKYN FEYS\VVFNMVLWIMI\ALALA\VIIT SYNIWNMDP\GYDSIIYRMTNQKISE WIECYLWPRIRKRGFGNWLFC
3192	8689	A	3452	3	371	MLPLARCSSSCLAPLSTYQTQVKTQ VHTETCI*MFIAALFIIVRR*KQPKCP SENK/WNKIWHIHTMK*YSATKKN KVLTYATI*MNTENMLSQRSY*QKT T*YLFLLMYMKIQNREMYRYKVD
3193	8690	A	3453	2	318	ETESRSVAQAGVQ*RNLSSLQ/PLPP GFK*FFSLSLRSSWDYRCMHDA*LI FLFLVETGFCHASQAGLELLTSSDPP ASASQSAKITSMSHHALPLFSNKVT FWDSW
3194	8691	A	3454	33	504	GLHNFLTYKATIISAVWYAVRVEN RSTEQNRVQK*TYMYVVKDAR*VN GNRILF*YC/WNN*IITWRKMNLNL DLTLHRKVYLKWVIDLNVKAKTVS PLGQNITESLHNFGVGKYFLDT*SI/ MPHKFFFNKLDIIRIKIFCS*KDAINK MKKWPGVVAH
3195	8692	A	3455	16	1011	WPVRAQAGQRPVLHTQVASLFAGV PCVLSHPKKGLLVPPFPPSKKGHLG KPHCPLPSAGRGAAGLGPLAQQPVS PAPASPMAPCKPKGLPPLPMGVEPE ILATMPVLTSHPP/SPEPMQSGNMPP S/PPSLCAFVPRWSHPPVPGWARWS CP/ALPAAPPSL*HWTRMQPPFCVPL RVPWVPSSGARGMKESGLDGQGFL GPTPSASPWGPWFDIRLPGCKQGIL AFKVTGPPTGFPDFEGKRFKKENKP PG*LESKAPDTVK*NPPSTNPPPAPA FLTWDCGAYRGPAGFLLVCQPSLLS LILKNIDDTLKCVERFEKLTASKQP KATVVLARRS
3196	8693	A	3456	1	348	PQQLRCFSFWRKDTKVDWLLLNRG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ARWLEKKTRLHRGPWARPRLMRA QREEALRREGGNPPPRGPGGEEAPL LRSSSGRPAR/HQT*QKSGASPSDPR SASR*ALRREGGNPPPRGPGGEEAP LLRSSSGRPARLRPSRSPERHPPTLA PPPARPSCPALPRLSMSAG
3197	8694	A	3457	2	247	PGCTILAHCNLCLSGSSDSPASAS*V TGNNRHAQPCPGLI*RTGFCHVG/R MNMLVFNSLTSSDPLEVST*GPQPP KVLGLQA
3198	8695	A	3458	1	515	GLGSLGPPAAVPTCPPRSPPP/GSPE GALQCGTLPAGTATPDGHVGWAVP FPPTVAPTRRSPRSPPQSC*WGLQH QLCPGSMEEMHTPHGLALPGASHIV PPTLCAPGGSEGARGI*PPA*AGYAL SLPTQFQTLILHPSCCRPGVP/PINLA AQLPPQVPHAPHAWQLPSAPK
3199	8696	A	3459	2	223	IYISPKALKFCREVGPICPPPK\KGSF PKIPR*QIFPFPRC*KTGKGQGIKRPP IRGKVLRCKPGLNLGPPRVL
3200	8697	A	3460	2362	2696	
3201	8698	A	3461	1586	2325	SPQRSGAARARPAPHRALLGRVPA RDAGSGRRTRSSRTRCGGCARRWS SISRRRRSSETSAGSWRRLSKPSGPG RWRHCARNTGRRCRPWWQISVVP RPSSRP/WLAALEAELKDSGEKPGK GASRPEDLQLIGRLQTRLKEREDIIK QLTKKKVEDVPSRVVSVPNLASYA KNFLSGDLSSRINAPPITTSPSLDPSP SCGRTYKPNQSTDAKTATRTPDGET AQAKEVQQKQGSPHQEWFTKYFSF
3202	8699	A	3462	125	489	YYLFFFFFFFLRQSLTLVAQAGGQW RNLSSLQPLPPGFKRFPCLSLLSSWD YKCPPP/RPG*FFVFLVETGFHHVAQ AGLELLTLGDPPTSISQSAGITGVSH QARPD*ETLEFQGDRVNLEE
3203	8700	A	3463	1503	1511	LFPVPFACPSLNCPSPPPIGVHLPIG*I QRLETPP*EEGRWIPRRTCGPARPGP PPGAPSVTLPPRTVHFGHPAKGIHFR KP/RHPG*CVFILTLD\CVHLH*KIND FIDTNFAMKSGYPNRIVRISFCLIHT
3204	8701	A	3464	54	593	RTALPAQHVASTWPGRPSRLLLRG GPGAPRSMQTGDSVGRGASKEPN*\ PHSGLPKHPLARSPPQRPSHRAMGQ GSPMPAGPT*TCAQALPPPSQDGLD LGNRAGWGCSPECLSKAPGGEGPA QAHPGPNPHTYRKPQWCWKLSPGH ALAPSPPRREVALLNLYSFIVPRDSP RPCIISL
3205	8702	A	3465	2	324	FFFFFLKWSLA/SFAQAGVQWCDLG SLQALPPGFTPFSCLSLLSSWDYRRP PPHLA/NFFVFLVDMGF\TVLARMV SIS*PHDPPALASQSAGITGVSHACP AYNVFKDDG
3206	8703	A	3466	142	413	AQEFKTSLGNMAKPCLYKKYKKM SWDYRRPSPRPANFSC\FLVETGFCH VAPAGLELLGSSNSPT*ASQSAGITG

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						VSHHTRPQIFLLPLSN
3207	8704	A	3467	241	523	NISGSFCMPILTAPLFTVAKRWKQY VPISG*MINKMWYIHTVEYYSASKR KIR*/PCAATWMNLEDMMLSEVSQS LEDKYSMLPFM*SIYVKYLEQSNA
3208	8705	A	3468	137	382	NSAVHQKFISIPNTSLPHSLAILKPQI NSLEEET*PFWCKKSSPVPKMRGER NDDNFHKVLLNVTNVDKPQGLRSP KWFCWG
3209	8706	A	3469	2	363	FFFDTESYSVAQAGVQWHDLCSLQ PPPAGFKQFFCLSLPSSQDYRHALP WLANF*FLVETGFHHVGQAGLKLL TSSDLPASGSQSAGITGMSQRTLQQ LSLKTTELRNFRCVPYCIINA
3210	8707	A	3470	135	466	GIDTILTLNQN*SLKTRQ*FTLIIF/IFF FFLRWSL/DSVAQAGVQWRDLGSL QAPPRGFTPFSCLSLPSSWDYRRPLP RPANFFYF**RRGFTMLARMVSIS*P RDLPAEFL
3211	8708	B	3471	27	21189	MKVSAARLAVILIATALCAPASASP YSSDTTPCCFAYIARPLPRAHIKEYF YTSGKCSNPAVVFVTRKNRQVCAN PEKKWVREYINSLEMSMICSGHHV YPNLPTDSFPGLDQFRGNYLHSRDY KNPEAFKGKRVLVIGLGNSGSDIAV ELSRLATQVHDVKVLGNKPKVIIST RSASWVMSRVWDDGYPWDMMYV TRFASFLRNVLPSFISDWLYVQKMN TWFKHENYGLMPLNGSLRKEPVFN DELPSRILCGTLSIKPSVKEFTETSAV FEDGTMFEAIDSVIFATGYDYSYPFL DETIMKSRNNEVTLFKGIFPPLMEK PTLAVIGLVQSLGAAIPTADLQAW WAAKVFANSCTLPTTNEMMDDTD EKMGKKLKCPYQFRLMGPGKWDG ARNAILTQWNRTVKPTRTRVVSEV QRPHPFYNLLKMLSFPLLLLAVTLT FY*
3212	8709	A	3472	9	339	ITLSLLSFFNLRPSFALLAQAGVHW RDLDSLQPPPLRFK*FSYLKSP\RSW DYGHAPPRPANSVLLVETGSLHVSQ GGLILPTSGDPPASASQSAGITGVTN CARPPSLFS
3213	8710	A	3473	1	50	
3214	8711	A	3474	1	1256	MAAAAAQGGGGGEPRRTEGVGPG VPGEVEMVKGQPFDVGPRYTQLQY IGEGAYGMVSSAYDHVRKTRVAIK KISPFEHQTYCQRTLRENQILLRFRH ENVIGIRDI\LRASTLEAMRDVYVVQ DLMETDLCKLREKPSKLSNDHILLT FLLPDSLAGPSSYIH\SAN\VLHLRS* SPPTWLIQHHLADLKVCGFG\LAGIC RSWRHDHTGFLTE\YVATRWYRAP EIMLNSKGYTKSIDIWSVG\CILG\E MLSTRAIFP\GKHYLDQLNHILGILG\ SPSQEDLNCIINMKARNYLQSLPSK TKVAWAKLFPKSDFKAL\DLLDRM L\TFNPNKRITVEEALAHP\YLEQYY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DPTDEPVGEGSPSPFGMEL\DDLPKE RLKELIF\QET\ARFQPGSAGRPPSPR QTSLHPGGWTCPPARPLSRRDC
3215	8712	A	3475	877	1463	LPFTAWP*E/QLQQAVHAGLPQQAK ILFDGGSEIGKILPAFQSGNLSCQLH **IGQRAGRGGLRIGRQGGFSFHQ* DGQQLIALH/QPGPERVAASGPRWF APAGENPV*WWFRNRQNPLIALRSL PAFQSGNLSCQLH**IGQRAGRGGL RIGRQGGFSFHQ*DGQQLIALHRLA LRELQQAVHAGLPQQAKILFDGGSE IGKIPV*GLLRWPPLPRDVQWDSAP LLRARWGL*GER*PREVPAALQGE* PQALLPGGGEPGWQPAEPHPAGGV HRAGPPGGGCWARAGGHQQKHLL RPAAGVPPDRGCLLQLGQIPH*AGE QVQAGPGTGQPAGEQAQRGLSGNA GPHQVPAEGDTGHLCGD
3216	8713	A	3476	29	1076	EQRDPQDIFSQRKSSAFPPSPEIEILS GGKSLSLQLHTPSPG/QQGETPRGG QQSQH/PCQGPGGGVPRYACAGGV PVTERGAQGWVHPALRRARYPDA GVQSHMKPAGDWGPGSNKPAGTD ADAVSGRR*LPKTLPSLGLGKKSPP GVPGHPEYPE/HGGSEALLHEFLLPP VSRLL\HGPLYPQMSNGTLHHYFVP DGDYEENDDPEKCQL/PLQGE*PQA LLPGGGEPGWKPAEPHPAGGSSPC WAARWEDAGRVLGGHQQKHLLRP RRGRELWQVPAAGVPPDRGCLLQL GQIPH*AGEQVQAGPGTGQPAGEQ AQRGLSGNAGPHQGPAEGDTGHLC GAQGLIRAAGPHH
3217	8714	A	3477	3	591	ERNYLFFLRWSLTLSSRLRGQWRN LG*\MQPPPP\GFKA\FSCLSLPSSWD YRRMPPCPANFCILVEIGFHCLAKL VLNSRPHDPPTSASQSAGITGVSHR AQT*KGIHLNELCTALAKEGRAWS GR*RAGAATPAP/PAPFTL*PGCIPES WPSPMPPPHLPLTALCKATHAGTK HPHLTKTVSSCGAVLQPTPQRKD
3218	8715	A	3478	1	235	RDHPGQH/GETPSLRKIEILAGHGVR HL*SQLLGRLRQENCLNSGGRGCSE PRSCHPTLAWAIEQGSVSRKEGHFP RLA
3219	8716	A	3479	2	928	RPPRPGTERALPSRLRSRPRVRTETP SPSSSGPPPSRSNTGMAPLRR*RV*R GTVPRSG*KGR*PCSRRRRSVPSGR TPALRGTRAPSDQGKGKARPPEP\P APSRPCPGSRFCRASRSRTSPRPPTP ARESGNPGRSP\DGGEKAAAQGS*K ESAACSNRAWS*WAA\SPPWITVTR QKRRGTLDQPPNQEDKPGARTLKS EPGKQAKVPERGQEPVKQADFVRS KSFLITPVKPAVDRKQGAKLNFKEG LQRGISLSHQNLAAQSALMMEKEL HQLKRASYASTDQPSWMELARKKS QAWSDMPQIIK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3220	8717	A	3480	1	435	EKINKIRWLPQQNAAHFLLGTNDK AIKLWKISERDKKAEGYNLKDEDG RLRDPFRITALRVPILKPMDLMVEA SPRRIFANAHTYHINSISVNSDHETP\ NIVDIKPANMEELTEVITAAEFHPH QCNVFVYSSSKGTIRLCDMR
3221	8718	A	3481	204	397	VPILKPMGSYG*EASPR\RIFANAHT YHI\NSI\SVNSDH\ETYLSADDLRINL WHLEITDRSFNIV
3222	8719	A	3482	1	1462	PLRSWLPRLPDSQADIISTVEFNYSG DLLAT/GDKGGRVVIFQREQEVLAQ PRRPALP*SVSSFLSTSCREVWQGCE FSLPFRERIK/GRPHSRGEYNVYS/TA FQSHGTGGFDYLKSLEIEEKINKIRW LPQQNAAHFLLSTNDKTIKLWKISE RDKRAEGYNLKDEDGRLRDPFRIT ALRVPILKPMDLMVEASPRRIFANA HTYHINSISVNSDH\ETYLSAR*PGGI NLW\HLGNHR*EAFNIVDI\KPANME ELTEVITAAEFHPHQCNV\F\VYSSS KGTIRLCDMR\SSALCDRHS/KSFFE EPEDPK/SSRSFFS\EIISSIS\DVKF\SH SG\RYM\MTRGLPVRWKVWGPSTW EEAGPVGGPTRVHEYL\RTKL\CSL\ YENDCIF\DKF\ECCWNG\SDSAIMT GSYNNFFRMFDRDTRRDVTL\EASR ESSKPRASLKPRKVCTGGKRRKDEI SVDSLDFN\KKILHTAWHPVGQCYL PWLATN\NLYIFQDKIN
3223	8720	A	3483	603	659	MCGFFFVFFFWRRSL/DSVTQAGVQ WRDLGSLQPLPPGFKRFSCLSLPSS WDYRRPPPCLANFLFLVEMGF/TTV LARLVSNS*PRDLPTSASPSAGITGV S*HASSRL
3224	8721	A	3484	84	202	
3225	8722	A	3485	3	577	ILGFPFFVRWGSHTVAQAGVQWCD HGSLQPRSPGVK*SSHLSLLGSWNH RHATTTPG*FCFFSRIRSHCVAQAGL *LLTSNHPPALASQT\VGITGVSHWT WPNTGFSVLTATNKNLKFFHYAISK CLVRAKLSSRLLKIEERNKALSAPV VSVSIFDRVLRLLGYSASDWQPEFV ETAVSNFVIYGIFRGQ
3226	8723	A	3486	3	248	SLYIEIPGGALPEGSKDSFAVLLEFA EEQLRADHVFICFHKN\FSFLGFEIV RPGHPLVPKRPDACFMAYTFERESS GEEEE
3227	8724	C	3487	185	340	MDNFCSSLCDFCHQNKNLRLVXXX XXXGGRFKGPLEGPKFTRACNELV FSL*
3228	8725	A	3488	1	546	NDRLN*TRELTSHERRRFPRPSSRLT DAQ\RINWRQVLSAGS\LYI\EIPGRR AAEGGARNSFAVLLEFAEG\QLRAD HVL\ICFHKNREGQKPPLL\RTFSFFG LEDFEDRGNPLVPKETPDACFHGLT TFERE\SSG\EEEEVGARLRGLGQFP RPGAHPLVKPGWGKEPVDSPHLAL GLSPML

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3229	8726	A	3489	1	526	FFFLERDPCSVTQAGMQWHDLGSL QPPPPGFKWFSCLSFPSSWDYRCPPP HPANFCIFSRD/MGFTILARLVSNS*P HDPPTSASQSAGTTGVSHSAWPVC/ LFEIEFHS\VAQAGVQWRDLGSLQP LPPEFK*FSCLSLPSSRDHRHLPSLPA KFHIFSRDRVSPCWPGWS*TPDLR
3230	8727	A	3490	276	735	FFFFFFLRQSFSLVSQAGVQWHNLG SLQPPPPGFRQFSCLSLPSSWDYRHP PPCPANFCIFNRELIIVYLIKTGF/IHV GQAGLELLTSGDPPALASQSAGIPG MSHCAQSTH*FLLAQQLFCSIYPSFH AQGVIPRIVTHKRETGSQTLYSIV
3231	8728	A	3491	2	344	FIFIF/NFLRWSL/DSVAQAGAQWRD LGSLQGPPPGFTPVSCLSLPSSWDY RCLPPRPANFF\AFLVETGFTVLARM VSIS*PRDPPASAYQSAGITGVTTAP GLLF*INICLAAFYFV
3232	8729	A	3492	109	559	QFLHRLVHDSGEVWMKLVE**NTL LAKMVSISWPRDLPASASQSAGITG LIGALVLSVGIYAEVER/HEI*NP*KC LPGSSHHPHPPGRRHVHGLLHWCA GVPP*QPGKH
3233	8730	A	3493	1	593	ETESRSIVQAGVQGRELGSLQTLPP GFTPFSCPSL\SWDYRHPPQHSANFL AFLVETGF\TVLARIVSIS*PHDPPAS ASQSAGITGVSHHARPQTGRFLLFL FFFFETESCSVTQIGVCSGHDLGSL\ QLRPPGITPFSCLSLPSSWDYRRPRL RPANFFFFVFFSRDGVSLC*PGWSRS PDLVICPPRPPKVLGLQA
3234	8731	A	3494	3	484	RFFFFFLRRSFT/SVAQAGV*WHDL GSLQPPPPWFR*YLCLGPLNSWDYR RGPPRLVNLCIF/M*R*SFTVLARLV SNSWPQ/CDLPP/SASQGAGNTGVS HCARPDEIFYYQC*Y*ETEMVRRST TQDRAGSTTVLKLLGQLRPEREIVN LALGALVYRNITPN
3235	8732	A	3495	104	288	GEVICGRRRSEVSRCNLVDLEPKGP WGHWQGG*GDRRAGGTP*GE/GHL RKKAI*GLQVQPGRPRTEGPLGA/PG KGDP*TPTEGPRGDARNCDACPRPR ARPVLVW
3236	8733	A	3496	3	641	RPPFFFFFFFFFFFFFRRSL/NSVTQAR LQWHY\LGSLQAPPPGFTLFSCLSLP SSWDHRRPP/RMPG*LFFAFLVETGF QRVSQGWVSIS*PQ/CDPPASGLSKC WGLQGVSHLRPSHLSFLAFSFFSFET GS\FSVAQAGLQWA\NHSSLQAPSP GFTPFSCHSLPSSWDCRHPPPRPANF /CCIFSRDGVSPC*SGWSRSPVLVIRP PRPPTVLGSQG
3237	8734	A	3497	1	296	VSRRFKQSIPP*AS*GWDHRCVPP\S LANFFFLLEMG\FPMLPRLVLNSWA QVILPSQPSQSAVITGMSHCACLYW LLKTKQIKIKQTGMSKVIKLFPL
3238	8735	A	3498	1	347	KKTGRRKRNMIDYEKKKNKEQEER

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RKKRKKRKSSSSSSSSPEEKKEEKK\K KREEEEENRKKEEEEE*DK/KEEED RRKHESRRRLRAVGDEVINKVCQE LKRTIPVGRDYRPLDPSS
3239	8736	A	3499	2	286	PQPCSLAPNPPRMPPGSF/TPCPSPPR SNITL*KQRPPSPPPSPEPPR\AQQRV AQNLTSPRPAAAKPPGWLSTNLSK ALPETPTVAQSPVLFTHF
3240	8737	A	3500	3	954	RPRAGAAGGGGGGSRPSGAHPSRS AC/GCPAGTRPGRAPPAASARPSRS KRGGEERVLEKEEEEDDR*R*R*RR SMCQRRSEVAPSSDRPGRCPAPPSL TASGDLRVPRRGSRSGPP\GTAPGPG *RAGASPGQRHPPGCSPWQP*TRKG EQVFFSFPASVATGPDSPSPVPLPPG KPALPGADGTPFGCPPGRKEKPFDP RSSWNVMGFRSNILLEA*FPEQATA FPRAGN*WQIFAAHAAHRCASPACP S\PRASPENLRAPHQGASARPL*GM MDPDGFL/ALSAQPHPCPKPIPAPISP KIPQSPGSWTGDTLSPH
3241	8738	C	3501	68	199	MPIIPALWEAQAGGLLRPGVCDQPG QYSKTSSLINKLKNPPSL*
3242	8739	A	3502	11	520	IRVDDFVAAHSRCCVAFPSSFTPRSR RRPKRRRRRRENDPAASSLPPAHLP CSVSQSAAGARLVLRPRACGAQAQ RP*LASGLRTSALRRRGHPRAELRS GPQRRQASE/PSPRGVAGARWWRR EDG/RPSKRSRMAQREAQQRTSPQR GNGRPKTSEKCPPEEKAVCRTPG
3243	8740	A	3504	78	595	NQNRLKEAGWRLKLADETSSSSHQ QVCGTHHVSAKCYS\GSPYS*KHPD SPSPATSRKQNLSTQSCISPMWPCSQ RSICQFGHGGTESGQGILLGLLRKAI GSPGKRSAPVQPNWEGGNG*EAAW ASSSSPSCKVTAPLAPSELFPSKFLL RNKKAQRKISHLLEVTVGHLLC
3244	8741	A	3505	2	267	ADLSAEAL*TRREWDDIFKVLKTSS/ LGQPKILYPSKLSLINEASSSSSSSSS SS/REFTTRLVL*EMLKGILHMEAQG QYLPS*KHTKV
3245	8742	A	3506	1	323	IAGEVNTPRSVTDRSS*Q/IIQEGIVQ LNSAIH/QTGCTNINRILPLTTAEYTF FSHLYRTFT/KIAHILGHMTHLNKG KRIEIIQSMLSDHNGIQPEISNRKIAG KSPNT
3246	8743	A	3507	3	814	SSGLAGTPPFPSEGAVCRSQPG*GSG \SPPLPVGPACWYLPCGP*DQRCPPG SLGPSAEPGS*NLSCPGRPMCSPAGT SCPAPV/PDSVTPVLRARGTACLPSP TFPAWSVPRFQPGAAPSSADLVHFH AASGPSASLSSSLSTKAPSLPLGACL PAGGVT*LFGPPSG/RLWRPP*GLTG GGLVWAAGVHWACLWPGQASGG SIRHVCVAVGVQGAPAQKEGGAGL GKGLGSFACGRPHLPPAYFACGRPH LPPAYFVLDLPFAKVLRNINI

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3247	8744	C	3508	112	252	MFRSMYNXXXXXXXXXXXXXXXX XXXXLGMSXXXXXXXXXXXXXXXLG F*
3248	8745	A	3509	448	715	FFIISIKIIEFFFFFETESCSSVTQTRVQ WFDLGS\LQPPPPGFKQFSCLSLSIS WHYTHVPPHLANYRIFSRDGV*PC WPGWSQTHDLE
3249	8746	A	3510	55	295	SQYAYTKEMESIVNNLPKKKTPGL HSFTGEFYQTFKNEMIL/YIL*FLPEI* SRG/IYPSSSSSSSLS*LPKLDKDIIRK EN
3250	8747	A	3511	2	853	DLMCKKMKHLWLFLLLVAAPRCV LSQLSSSSSSSSSSSSSSSSSSSSSSSS DSVRHNSYYWGWVRQPSGKELEW IGSLYFTGTTHYSPSLKSRVTISADT SENQFSLTLTSVTAADTAVYYCARP RNIVGSSSSSSSSSSSSSSSSPSTKGPS GFPLAPSSKSTSGGTAALGCLVKDY FPEPVTV\SWNSGALTSGVHTFPA/V LQSSGLYSLSSVGTVP\SSSFGHPRT YI\CNGKSQSPATTKVDKGELSPK\S\ CDKNSTHAPPGPQHLETPWGGPVS LFFFPPKT
3251	8748	A	3512	3	2310	QLLTMDWTWNILFLVAAATGAHSQ VQLVQSGAEVKKPGASVKVSCKAS GYTFTNNGLAWVRQAPGQGLEWM GWTIASNGKTNYAQKFQGRVTMTT DTSTNTAYMELRSLRSDDTAVYYC AREKDNYATGAWFAYWGQGTLVT VSSGES*AWYPGIQICSMLEL*ISAF WGRPGLTLAGGREGAKVTQVAPA RCTPNAHEPRHWTLHGPSRIDKNR GASAPWAQLCPTPRSHGTTSLAAST KGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKR/VW*EA STGREGVCWKPGSALLPGRTPAVQ PQPRAARHAPSVSSPGGL*PPHSCSG RGSSGFFHQAPGRHRLDAPTPGPAH KGAGAGLRPAKSHIREDPAPDLSPP QRPNSPLPQLGHLLSSQIPVTPNLLS AEPKSCDKTHTCPPCPGKPAQASPS SSRRDRCPRVACIQGQAPAGC*HVH LHLFL\APELLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGGTRGV RGPHGQRPARPTLCPESDRCTNLCP YR\QPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHY TQKSLSLSLGK
3252	8749	A	3513	1	1677	AEVQLVESGGGLVQPGGSLRLSCA ASGFSFSKAYMNWVRQAPGKGLE WVGRIKTKKDAGTTDYAAPVKGRF

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						TISRDNSKNTLYLQLNSLRAEDTAV YYCAKDEFSSTRKNFLTGQSKTFAA YYGMDVWGQGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVL QYSGLYSLSSVVTVPSSSLGTQ\TYT CNVNHKPSNTKVDKTVELKTPLGD TTHTCPPCPTP*L\LGGPSVFLFPPKP KDTLMISRTPR\VTCVVVDVDPRKT PEGQVPTWYV\DGL\EVHKCQDKSR GKEQYNSY\YRVV\SVLTVV\HQDW \LNGK\EYK\CRVSHKSPPQAPIEETH LPKPKGSPQNPQVYTLPPSRDELTK N\QVSLTCLVKGFYP\SDIAVELESN\ GQPGNNFK\TTPPVLDSDGSFFLYSK LTVD\KSRWQQG\NVF\SCSVMHE\A LHNPYTQKSLSLSPGKMIPTADKPP LPGSLAGRTKDAWHGTPVYILPRAP KHGNKAPTPWPWAKKKKKKKKKK KGGRSRVSLEGPKLTRTQLS
3253	8750	A	3514	1	164	TRVNENQIESKAAYALFYKRQDVA RRLLSPAGS/SGAPASPACSSPPSSEF MDVN
3254	8751	A	3515	1	712	EILIIHLKRFSYTKFSREKLDTLVEFP IRSGARERMAGGRQGKEGVYQY*P SPHPQ\DLDFSEFVIQPQNESNPELY KYDLIAVSNHYGGMRDGHCMCQA VGGACPGGSGQGGDQDLPSE*LGM *ASGEGSSVVGRK*TRSEIWTLSEEA RKGRRG*LSFPFR\TTFACNKDSGQ WHYFDDNSVSPVNENQIESKAAYV LFYQRQDVARRLLSPAGSSGAPASP ACSSPPSSEFMDVN
3255	8752	A	3516	3	3090	IPLLQLLLRRLWRRHGRWTEDREPQ HEELPGLDSQWRQIENGESGRERPL RAGESWFLVEKHWYKQWEAYVQG GDQDSSTFPGCINNATLFQDEINWR LKEGLVEGEDYVLLPARAWHYLVS WYGLEHGQPPIERKVIELPNIQKVE VYPVELLLVRHNDLGKSHTVQFSH TDSIGLVLRTARERFLVEPQEDTRL WAKNSEGSLDRLYDTHITVLDAAL ETGQLIIMETRKKDGTWPSAQLHV MNNNMSEEDEDFKGQPGICGLTNL GNTCFMNSALQCLSNVPQLTEYFL NNCYLEELNFRNPLGMKGEIAEAY ADLVKQAWSGHHRSIVPHVFKNKV GHFASQFLGYQQHDSQELLSFLLDG LHEDLNRVKKKEYVELCDAAGRPD QEVAQEAWQNHKRRNDSVIVDTFH GLFKSTLVCPDCGNVSVTFDPFCYL SVPLPISHKRVLEVFFIPMDPRRKPE QHRLVVPKKGKISDLCVALSKHTGI SPERMMVADVFSHRFYKLYQLEEP LSSILDRDDIFVYEVSGRIEAIEGSRE DIVVPVYLRERTPARDYNNSYYGL MLFGHPLLVSVPRDRFTWEGLYNV LMYRLSRYVTKPNSDDEDDGDEKE

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DDEEDKDDVPGPSTGGSLRDPEPEQ AGPSSGVTNRCPFLLDNCLGTSQWP PRRRRKQLVQLQ\TVNSNGHNRLH HSPCTKSNAKPVHCYSTWKP\EMK K\RYYDE*EGEGLREGNAFRRGYV* RKAPVRLQECIELFTTVEPPPFGGK\ EREKPW\YCP\SCKQHQLAT\KKL\D LWM\LPEILIIHLKTFFPYTQVLPEKK LEHPSWKFPYPGTLDFS*/EFVIQAH QNEVEIRELYK\YDLI\AVS\NH\YGG MRDGTLTQHLACNKDSGQWHLLLI DNSVFPLFN*GIQIRVPRAAYVL\FY QRQ/DTLARRLLSPCRAHLAPSVLP CLHAPSPQLVSSCDVILRALGPAPE KKKKKALSAISLLVSAPLLLFVLGA PARHCRLSRGYCSPVPLNRSLPGKN RSCLLLAVRAPPCVCPSSSDPPF
3256	8753	A	3518	1	271	PLPPGFK*FSYLRLPSSWDYRCPPPH PTNF*FLVAMWFCHVGQAGFELLT SGDPPTSASQSAGITGVSHRSRPIVD FLNYLLRKSYPFT
3257	8754	A	3519	3	633	FFFI*DRVSLIAQAGVQWRNCGSLQ PPPTGFKQFSCLSLWRSWHYRCRH HAQLIFVFLVKTGF\TMSVKADLEL LTSGDPTASASQSAG\ITGVNHQCPA SKQF*FHCKSW/CLF*MQSLSFFFLG GGQSRSVGQAGVQWHDLDSLQPLS PGLKQFSSLSLPSSWDYRGVPLRLA NFCIFSRDGVSLCWPGWS*TPDLKA NPTRLGLPKGWGL
3258	8755	A	3520	2	430	CLKNMVGAGEVDEDLEVETKEECE KYGKVGKCVIFEIPGAPDDEAVRIF LEFERVESAIKG*WYS*ILKNKKVEF TALIFTSKAYCLIKVKPLSYRIPALF CLLFAFQRLLTLNGRYFGGR\VVKA CFYNLDKFRVLDLAEQV
3259	8756	A	3521	3	1076	HEERQRQRELERQKEIEEREK\RRK DRHEASGFARRPDPDSDEDEDYER\ ERRKRSMGGAAIAPPTSLVEKDKEL PRDFPYEEDSRPRSQSSK\AAIPPPVY \EEQDRP\RSPT\GP\SNSFLANMGGT VAHKIMQK\YGLPGGPRVLGKHEQ GLSTALSVEKT\NKRGGKIIVGDATE KDASKKSDSNP\LTEILKCPTKVVLL RNMVGAGEVDED\LEVET\REECEK\ YG\KVGKCVI\FEIPGCPLMMEASTG YFLEI*EELNSAIKAVVAL\NGRYFW CTGW*KAMFLQIWAKFRVLDLARN QVWIFKEPRARVISGDPLNELQAVE KKKEKGPQPPWLFAYPRLLEGLLRY MLIDPFFYFVVF
3260	8757	A	3522	1381	1787	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3261	8758	A	3523	1147	1553	.LEYVAHPLHQLLILNNFYSVLNEKY

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						LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3262	8759	A	3524	1456	1862	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3263	8760	A	3525	889	1295	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3264	8761	A	3526	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3265	8762	A	3527	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFFCS/RD TVSLCYPGWSRVA*SRITATSA\PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCLSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFIYLFIYFHRDEGSLCCPGWS* TPELK
3266	8763	A	3528	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3267	8764	A	3529	10304	11097	FAFSPK*HSCLRCPCI*FSSGLLHEVL *LLPLCWP*THGWDPGSREANKSPK LHAIRCVWVLEEENLWLSSNSQSLQ TVKN*ESHIN*SCRSNLI/HH*FWNQ VK*K*LLNISGNCFFFLRWSL/DSVA QAGVYWRDLGSLQPPPPGFKRFSCL SLPSSWDYWHLPPCLAKFCIFSRDG/ GFTIWARLVLNS*SCDLPASGSQSA GITGVSHHTW\LQVTYFLKEMRSCY FSQVGWPQTPGLKQCSHLKLLSSW DYRHMSPHLAISGS
3268	8765	A	3530	87	411	ARLVQNTVAQLKEVQYKLFFGFLF FE*/QSHSVAQAGYSAVIIAHCNLSL

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						LGSSDPFFSAS*VAGTTGMCQHAW LIFDR*WR*GLAMLPRLEM*IFLISH LRLIWSAWS
3269	8766	A	3531	31	403	THLNGLQIRGSPLFFF/FELESSSVA\ RLQCSGVISSHCNLRLPGSSNSPASA S*IAGITGAHHNPG*FF\VFFSRGRFH HVGQAGLELLTSSDPPRPSTLPQSG WGFTRHGAIAPQWGQVPFHRS
3270	8767	A	3532	7	1047	
3271	8768	A	3533	3	53	
3272	8769	A	3534	7	960	
3273	8770	A	3535	1538	2287	WWSSSKLRLIYYYSLFFFFFFFFFG M*SYSVTQARVQWHHLGSLQPLPP GFKQFSCLSLPSSWDYRHPPHLANF LYF**RWGFTMLARLISNS*PQ/CDL PASASQSAGTTGLSHCAQ/LLFAFLT DNSVLIETALT*LQSCAS*KLN*IIPL ESSDFYTFFFETESHSV/TQAGVQCR NLGSLQPPPPRFKQFSCLSLPSSWDY KCTLPRPANFCIFTRQGFTMLARIVS PGSLGLMISLPRPPKVLGLQV
3274	8771	A	3536	3	263	LGVGDRVSLCHPVWSASSL*SQTPG LK*SSHLSLPSRWDNRHAPPCLA/SL KNFCRDRGLTMLPRLVSNSWAQAI LPPQLPEVLGLQV
3275	8772	A	3537	33	295	AGMQWCSLGSLQPPPPVLRRSSHLS LPSSWEYSHTC\NFCIFCRDGFAVLP RLLG*SNRPASSS*NTGITGVSHRAQ PSLFLSYSFFF
3276	8773	A	3538	3	33	
3277	8774	A	3539	1	375	
3278	8775	A	3540	3	340	HEVVAA*YY\G*PSIAQEVAGTLAE LDVTLQLLEDKFLQNKVFLTGPHIS LADLVAITELMHPAGAGCHVF*GLP TLATWRQLVEASPGEDLFQEVHEVI LKATDFPPADHTI
3279	8776	A	3541	30	284	YSVSTPLRDSPNPNHLSSLGHCPASS QTEPQAPQQALGQPATKLLPHPQPP /MPQPSSKP*VSATSLCTSPPLPPLCP AGGSSGTT
3280	8777	C	3542	127	435	MAASXNPEVLDITEETLHSRFLEGV RNVASVCLQIGYPTXASVPHSIINGY KRVLALSVETDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHHSCSXCCCSP S*
3281	8778	A	3543	3	417	
3282	8779	A	3544	2	881	RGKLCAYGRPPMMRRSIEGN/LENN PASEELLPH*\RGHLGFCFT\RED\LT EI\RDMLLA\NKV\PTAARCWCQLPP CEVTVPA\QNTGLG\PEKTSFFPGL* VSPTKNLPGGTH*KS*SYVQL\IKT\G DKMGSQTKAKAAEKMLKNLPPSPF GAGQPKQGV\RKNGKHPTNPESA*I STRGKLCHSRF\LGGCPANVAKCLS CKIGYP\TVASSTPIPII\NGYKRVPGP CLWTPDYTFP\LAEKVKAFL\ADPSC LCVLLPPVG\AATTACFALLLQPPA

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						KVEAKEESEESDEDMGFG\LFD
3283	8780	A	3545	2	311	DGVSLLLSPRLQWHNLGLLQPPPP* FKGFSCLSLPGSWDYRHV/PPCLAN FVFLVETGFRHVGQTGLELLTSGDP PASASQRAGITGVSHRTWQKMYFL SQKYF
3284	8781	A	3546	1	290	KTFFFFF*DRVLFCCPG*SAVAQ\SW LTAALTSWAQGSS*DHRLKP/HMLS FFYFCRQGLTMLPKVVLNSWAQAI LPPQPPM*PGLQACTYAWSLRAL
3285	8782	A	3547	229	486	IKIKINQAWVCACLSLPSSWDYRHG PPHPANF\FVFFLVETGF\TMRARLA SNS*PCDPPTSASQSAGITGVSHRAG CSEAFRSQV
3286	8783	A	3548	2	431	ARGSIYQNDTTI*NMYLDNRASECT VRELVKQK/R*MEKPTIIFGDFNNPV SLIEGSSK*KISGTMENLKNTANFT* LIFIKCSAQQHQNAHSFPV/PHRTF/S KIDHFLWCKRGLNKCKMIQIIQNVV CDHTALNKKPMPERSLEK
3287	8784	A	3549	2	194	VDFFFFFLRWSI/NSVTQAGVQWRN LGSLQALPLGFMPFSCLSLPSSWDY RCPPPAHPANFFLHF**RRGFTVLAR MVSIS*SHDPPASDSQSAGITGLSHR AR/LKGHYDF*EMAC/HLICKRGRQ VP*LFFFFFEMEYHSVTQAGVQWR NLGSLQALPLGFMPFSCLSLPSSWD YRCPPPAHPANFFLHF
3288	8785	A	3550	2	489	ARGTQALMMMT/GTACHASPH*GG RLTS*PGAICFTHGDMAA*WREESC LLVT/WDLVMSEGLGMRYAFIGPLE TMHLNAEGML\SYCDRYSEGIKHV VQTFGPIPEFSRA\TAEKVNQDMCM KVP**PGSTLAAR\RHW\RDE\CLM\R LAQV*RSSSCSPQLNFLC
3289	8786	B	3551	13	441	MEGVEEKKKEVPAVPETLKKKRRN FAELKIKRLRKKFAQKMLRKARRK LIYEKAKHYHKEYRQMYRTEIRMA RMARKAGNFYVPAEPKLAFVIRXR GINGVSPKVRKVLQLLRLRQIFNGT FVKLNKASINMLRDCRAIYCMG*
3290	8787	A	3552	1	775	RRVPA\VPETLKKKRRNFAELKIKR L\RKKFAQQML\RKAR\RKLIYEKAK H\YHKEYRQMYRT*NFEWARMGK KKLANF\YVPAEPQIWRFVIRIRGI\N GVSPKGSERFFQLLRLRQI\FNGNLL *KLNQGFRFNMAEDF*SPYIAMGGT PNLKVSKMN*SYKRGLWAKSNKK R\IAL\TDNAL\IARSLGKIRHILAWE DLIHEIYTV\GKRFK\EANNFLWP\FK LSFSTKVEMKKKTTHF\VEGGDAGN R\EDQINRLIRRMN
3291	8788	A	3553	1	356	SHHVQLLFEFFVEMGSPCVSQAVL* LLGSSDPPVLASENVGIK/GPPHPA* S*F*IIACVFVYIYFLEMGSCSFAQA GVLWYNHSSLQR*TPGL*QISLLSPL SSWDYRHVPPCLVIYF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3292	8789	A	3554	3	352	HEGFTMLVRLVSNS*HRDPQASASQ SAGITGVSHHANP/CFFLTESNWVA QAGVQWRVLS*LQPPPA*FKGFSCL SILSSLS/WGYRCLPP/HPANFFFF*K GFFFWFPSWNAMGKKWFN
3293	8790	C	3555	55	201	MPKNYPRLWWQHVCNPQPTWEAE VGELLEPQEAEVAVSQDHATALQP G*
3294	8791	A	3556	3	212	QEFFFFFFEM*SRCVT\RLEGSGAISA HCKLCLPGSCHSPASASQDSIFNTQ HLNVGRNSTSKSKPIDYF
3295	8792	A	3557	2	265	EKESRSVTRLECRGAISAH*NLHLP GSSHSPPSASHVAGTTGACTT/AQLI FFVFLVETGIHHVGQDGLNHL/NLVI RLPQPPKVLGLQA
3296	8793	A	3558	354	675	HFISYFPDGAELTSSIRVPFFYSNVLF FF/CRQESRCHQAGVQWHDLGSLQP PPPGFKRFSCLSL*SS*DYRQAPPRP ANFCIFNRGPVSPCWPGWSQSPDFV LVPNS
3297	8794	A	3559	1	1203	
3298	8795	A	3560	2	634	VNTEKLTAFVNTLNGKNGTGSHLV TVPPGPS*ADALISSPILAGESGAML GLGASDFEFGVDPSADPELALALRV SMEYQRQRQ\EEYARRAAAASAAE AGIATTGTEGERDSDDALLKMTI\SQ QE\FGRT\GLPDL\SSMTEEEQIAYA MQMSLQG\AEFGQAESADIDASSA MDTS*PAKEEDDYDVMQDPEFLQS VLENLPGVDPNNEAI
3299	8796	A	3561	506	930	IRTTQIGLCLSQVYFIVFDLHAQYEII KATNITTPTLSKIISIRPRRFIFPVT*L LNMFAFSSPMVPVSLSQRIGTI*FLF RFFNT*IFSDGLTNRLTCSRFANCKV NPVIGSISKYVLCSSSFGFNPSIGSET SGLAYRK
3300	8797	A	3563	3	271	FFLET*SCSVG\RLECSGVILAHCKL RFPGSSDSPASASGVVGTTGAHHHT RLFCIFSRDGFHHVGQDGLDLL/NL VIHPPWPPKVLRLQA
3301	8798	A	3564	1	218	ETGSPSVT\RLECSSIQ\SAHCNLDLP GSSDPPVS\APQVAGTTGTCHNTQLI FVFFVEMGFCHLSQAVLQLLG*T\IH PLWPPKVLGL*AQVILLSQTPQVAG TTGTCHNTQLIFVFFVEMGFCHLSQ AVLQLLG
3302	8799	A	3565	1	294	ASTFFFFFGDRVSLFLPRLEYNGAIS AHRNLC/LPGFSSDSPAS\AS*VAQD YRHAPPHLANFVFLVETGFLHVGQ AGLKLPELSVIHPPWPPKVLGLQA
3303	8800	A	3566	3	292	FFETKFSSVTQAGVQWHNLGSLQPP PPAFKRFSCLSLPSSWDYRHLPPRPA NF*FLVEMGFHHVDHADLELPTSS DPPTLASQSAGIIGVSHRARP
3304	8801	A	3567	3	389	
3305	8802	A	3568	1	672	
3306	8803	A	3569	1	2018	MSDNGVRTGAPSTDQRTGMSVRAE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WRRGEFLVTGRRPLVGGGAGEEGE LGGDARSSRDPELQSYAAFVAVVT RIWLPAPRCPALGGLASGPGKAEQF SRSLYLPDHLGEGNGGLLGKSLEPY RSACMSAAGLKITGSKETKRRLLLI SIDWSRDLMNLCIYFRVYCQEKQEE RRELPRIITGPPPEAAVVAFEWLKTS TLTGLHPQLPLSLPQPECALPYLVR AFSRGDYMGRIQEVGWVTAGLVIW AGTCYYIYKFTKGRAQSVRTLARN GSTVKMETVVGVQSQTLAINEAEIK TKPQVEIGAETGARSGPRAEVETKA TAIAIHRANSQAKAMVGAEPETQSE SKVVAGTLVMTEAVTLTEVKAKAR EVAMKEAVTQTDAEAGKIVKKEAV TQTKAKAWALVAKTEAKREAMTQ TKAETHILAEKETEINRVMVTQSET LAVPREVAKMGATNKTGIVDETKT RALEETVSVAKTQSEARPGATVDA RGNPNGMSREVAGVDMKSCAQSQ AVTKIQGDDMPGTGVEDMGNCKT MSRAESGADTRASAQPQIFAKTQTE AIPGAKIDAGGNTNAMCKVGAGAD VRACIQPQTVAKKQAEVTSGARVD GRGNTNVISKAITGADMRAAAQPQ AVASTHAEAMSDAKVKNRGNPNA MTKAGAKANLRANSQVEALPDAR DKSRGNPNVMAKVGDGTDMLSCT QPQLVASVQADTLSDGKIKVRGNV NTMPKEGAGVDMKAQGMAQSQGE ALPNTRGKARGKAKAKCKTGPGM DMKTCTQPQAGVKTPAEALLDSRV DGRGNPNATSKAGTKADQRVCGQP LVVANPQGEALPGAKNKVKGNPHT VLKVGAGEGTTDSAQPEAVVSFQG EALLGTKNKVKGNPNVVLKAEVGE GAMGTAQLQIMASSKGEALLDSKN KVKGNSNAVSKAGAGTDTTGSVQP QIVANSQGEVLPGAKNKIRGNPTTV PNSGVGPYTTDSARLQAVANSQGE VLPGAKNKVKANLNAVSKAEAGM GATGSVQPQAVANSHCETLPGAKN KVRGNWNAVSKAGAGMDTRGSAQ PQAVANSQGEVLPGAKNKVKGNPN VVSKAGAREDTVGSTQPQVLASSQ RETLPGARNKVKGNSNVVSKAGAR EDTMGSAQPQVVANSQRETLPGAR NKVKGNSNAISKAEAGAGIMGSVQ VQVVASFQGEVLPGAKNKVRGNSN AVPKAEAGADTVGSAQPQAVANSQ SETLLGARNKVKGNTIAVPKAGTG AGTRHSAQPQIVAGSQGETLPGARD KSMSTSEAEATAEDEAYAKPEAEA MPTSESEGGSGTQACRKTQPNIHDY YWNGIGVEDWIAAERWIKFRFQTM DGDWENSVSWADDENEASIGSWSG ASDKAGIIRSWAVACDETSVKSWA GARAENVVGIGTWARAGEQASGGL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WAGGQTSEGTWAGDKASGGAWT GAENQASGGSWALAGNQAIGELW AAGQASDGSWPGGQASGVSWVGE EAIGGSWTGAENQASEGSWAGAGA GNMSSVSYWAGVVDQAGGGSWA GTSDQSGGGSKPRFEDQASGEGSW AGAGGQASGGSMLGPEDQSSGRSW ADTADQASGGSRLGHVDQSSGGA WAGTLDQSGGGSKPRFENQTTEEG SWAGAGGQAGGGSKVGPEDQSSG RSWANSGDQISGGFLVGIVDQANG GSWTGAGHPASVGPKPIFEDQVSGR GSWADAREQVVGDSRLGLRDQSSG DSWAGTGDQASGWFCVCPGSQTN GGSWGGASGQDVGGSRPGPTNQSS AGSWDSPGSQVSGSCWTGAGAVD QAGGCSKPGFEDQAIGGGFWPGAG DQTGGGSRPGSEDQSSGIGSWGVA GGQVLGGARPGPADQSSGGSWAGT GNQSSGRSWIGPGDQAVDCSKPEFE DQACGGGSWAGAGSQASGESWAG SRPGNEAIGGSRMGSEDQATGGSW ARSEDQASGRFQVSFEVEANEGFW FGPGAEAVIGSWCWTEEKADIVSRP DDKDEATTASRSGAGEEAMICSRIE AENKAKSRLGAGEEAGVESWTLAR NVGEDELSRESSPDIEEISLRSLFWA ESENSNTFRSKSGKDASFESGAGDN TSIKDKFEAAGGVDIGSWFCAGNEN TSEDKSAPKAKAKKSSESRGIYPYM VPGAGMGSWDGAMIWSETKFAHQ SEASFPVEDESRKQTRTGEKTRPWS CRCKHEANMDPRDLEKLICMIEMT EDPSVHEIANNALYNSADYSYSHEV VRNVGGISVIESLLNNPYPSVRQKA LNALNNISVAAENHRKVKTYLNQV CEDTVTYPLNSNVQLAGLRLIRHLT ITSEYQHMVTNYISEFLRLLTVGSGE TKDHVLG*EQRSQCHD*SRGQGK LEGQFPG
3307	8804	A	3570	1	611	YAALGADVTRVSLPTPRCPALGAL ASGPGESGPTLLQDCGAKCPG/GPQ PRGENREKEETTRIGPGVMESKEKR AVNSLSMENANQENEEKEQVANK GEPLALPLDAGEYCVPRGKS*GGSA FRAAHP\EYRWDMMHRPWRTHRPR DEEKRIMEKDWGGGETADGKKLE GEKPVGVISLRGESGTDPPSPMTHH D*VFALLPLNP
3308	8805	A	3571	1	379	EMESHSV\TRLECS/GTILVHCNLCL LGSSDSPASAFQVAGITGVHYNA*V IFVF\LVETGFCYVGQAGLEFLTSTD PPASGFQNCWNYRDEKPHPAETVS KTTTTKNYICVSTINYKKKNLGLSNI L
3309	8806	A	3572	6	222	DRVSRSAAQAGV/QWC/NLSSLQPL PPRFK*FSCLSLPSTWDYRHTPPRPA NFCIFSRDRVSPCWAGWSQSLDLK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3310	8807	A	3573	1	445	
3311	8808	A	3574	1	3212	DSINNLQAELNKIFALRKQLEQDVL SYQNLRKTLEEQISEIRRREEESFSL YSDQTSYLSICLEENNRFQVEHFSQ EELKKKVSDLIQLVKELYTDNQHL KKTIFDLSCMGFQGNGFPDRLASTE QTEIMKDLSKGGCKNGYLRHTESKI SDCDGAHAPGCLEEGAFINLLAPLF NEKATLLLESRPDLLKVVRELLLGQ LFLTEQEVSGEHLDGKTEKTPKQKG ELVHFVQTNSFSKPHDELKLSCEAQ LVKAGEVPKVGLKDASVQTVATEG DLLRFKHEATREAWEEKPINTALSA EHRPENLHGVPGWQAALLSLPGITN REAKKSRLPILIKPSRSLGNMYRLPA TQEVVTQLQSQILELQGELKEFKTC NKQLHQKLILAEAVMEGRPTPDKT LLNAQPPVGAAYQDSPGEQKGIKTT SSVWRDKEMDSDQQRSYEIDSEICP PDDLASLPSCKENPEDVLSPTSVAT YLSSKSQPSAKVSVMGTDQSESINT SNETEYLKQKIHDLETELEGYQNFIF QLQKHSQCSEAIITVLCGTEGAQDG LSKPKNGSDGEEMTFSSLHQVRYV KHVKILGPLAPEMIDSRVLENLKQQ LEEQEYKLQKEQNLNMQLFSEIHNL QNKFRDLSPPRYDSLVQSQARELSL QRQQIKDGHGICVISRQHMNTMIKA FEELLQASDVDYCVAEGFQEQLNQ CAELLEKLEKLFLNGKSVGVEMNT QNELMERIEEDNLTYQHLLPESPEPS ASHALSDYETSEKSFFSRDQKQDNE TEKTSVMVNSFSQDLLMEHIQEIRT LRKRLEESIKTNEKLRKQLERQGSE FVQGSTSIFASGSELHSSLTSEIHFLR KQNQALNAMLIKGSRDKQKENDKL RESLSRKTVSLEHLQREYASVKEEN ERLQKECSE\KERHNQQLIQEVRCS GQELSRVQEELKLRQQLLSQNDKL LQSLRVELKAYEKLDEEHRRLREAS GEGWKGQDPFRDLHSLLMEIQALR LQLERSIETSSTLQSR\LKEQLARGA EKAQEGALTLAVQAVSIPEVPLQPD KHDGDKYPMESDNSFDLFDSSQAV TPKSVSETPPLSGNDTDSLSCDSGSS ATSTPCVSRLVTGHHLWASKNGRH VLGLIEDYEALLKQISQGQRLLAEM DI\QTQEAPSSTSQELG\TKGPHP\AP LSKFVSSVSTAKLTL\EEAYR/RGLK LLW\RVSLPEDGQLPLHCEQIWRNE RQRVPKLHKKLFEQEKKFAKTP*RF LQLSK\RQEKVIFDQ\LVVTHKILRK ARGNLELRPGGAHSRT\CSPSR\PGS ALATRKEHRNQQHSAEQASRNSWQ GGQRRHRKEPSLWLSKPCPSLRCPF SLTNTMVTNIPWKVIIHLICLIPPRQ
3312	8809	A	3575	1	1362	SGNIKVLERFLYIDTKFSQNRCQKA LPMAHSAYQSNLPHNYTMTVHNN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QLAQALRVYSQHAIGAVLYKYSMQ VHEDCYKFWSNG\MQLCEERSLTD QHCVHKFHSLPKSGEKPEADRNPPV LYHNSRARSTGACNCGRKQAPRDD PFDIKAANYDFYQ\FWEEKCCGKIG S\YSISQYLEPSTPGSWLLA*KWNP/ RPAPPDSDADKLKEKEPQTQGESTS LSLALSLGQSTDSLGTYPADPQ/DRR R*SRSSWSSRSEN/SRRDQTSLIDRH/ LTVEYLPGMLHSNCPKGLLPTFSSW VFVKLGPG*SYNFHTRFR/NQQGFIP GNKLSYALGTLSSRARSWR*RRLR HKLLACSK*SYSWKEKCGCNGKRK TAR*H\TRAFVGFEYEDSRGRRFMC SGALTK**K*WGSGA/IRDSAFKSP*I VDMPLYI\RHPLKVEGLKTLITLQL MRLFVVVPDASFAR
3313	8810	A	3576	1	673	EGGWMEDYDYVHLQGKEEFEMTH IELLDKGSITRQGMSQL*LEQLKLFV RLEQEVSRPIDHDLAIWTPAQPLAP GRSGG\LGPSDRQLLLFYLEQCEAN LTTLTNAVDAFFTAV\ATNQPPKILV GASKVVLL\SAHKLVFIGDTLSRQA K\AADVR\SQVTHYSNLL\CDLL\QGI VATTK\AAALQYPIAFPGPKDMV/E KRVKELGHSTQ\QFPPRS*GQLGSPP EGW
3314	8811	A	3577	3	531	FFLLQSL/DSAGQARVQWCDLGSLQ PLPPRFMRVSCLSLLSSWDYRHLPP RLAMIFVFLVE\QGFTVLARLFSNS* PQ/CDPPTSASQSAGITGMSHHA\RL FLFFETGSGSIAQGGVQ*CNLGSLQP LPPRLKPSSHLSLLSS*DYRRVPTCP SNFCIFGRDGVSPCCPDWSGTPGLK
3315	8812	A	3578	1	223	GSGGIHRLPLSSRPEQPIVWLWAPG CFSHLSRLQVTV*/GEIKQRCRELHH SLAQHPRHQAGNHISHPILHLKIL
3316	8813	A	3579	3	341	FFETESCSVSQAGVQWRDLGSLQA LPPGFTPFSCLSLPSSWDYRHLPPHP ANF/SVFLVETGFHRVSHDGLDLLT RDPPTSASQSAGITGVSHRARPIVAI FMFCEYPLFSSHF
3317	8814	C	3580	168	347	MTYGLLLFLGNNPHLNLYXXXXXX XXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXSTIV*
3318	8815	A	3581	852	1216	GFLINGNTDFFFFETESRSVAQGGV QWRDLGSLQPLPPGFKRFSCLSLPSS WDYRHLPQYPS*IFVFLVETGCSSIY STIL**RP\HVGQAGLELLTPGDPPAS TSQNAGITGLSHRTWSAI
3319	8816	A	3582	2	238	
3320	8817	A	3583	680	891	
3321	8818	A	3584	697	979	IFGVSQGYYKILWKMNSLPGVSFES KRSF*QK*LQILSS*FAKKIFYWHEN NRCKWRPNIPLKCIYSITSQKLFYPS LLFFPLLPTFLGVGGAR
3322	8819	A	3585	2	518	GRGYQNPGRQCTSDRLSEHVSEGES

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PPDSQEDSFQGRQKSKDKAATPRK DGPKRSVLSKSVPGYKPKVIPNAIC GICLKGRESNKERKG*IHFIHCSQCE NSG\HPSCLDMTNGACFYD*DLTPW QCMECKTCHICG\NPHHEEEMMFC\ DMCDRGYHTFCGGPGSNPTRPLNL
3323	8820	A	3586	1	165	SLEDRVLLCHPGTAYCSLELLGSISP PALTLTSEAS\LPGRDYREIPGSPCQL FL
3324	8821	A	3587	1	249	LVDRVLLCHPGTA/VLQP*TPGINQS SCLSLPSS*D\YRYVPPCLVYCFIFLA EMGLTVLPRLISNSWPQAILPSQPPK VLGLQT
3325	8822	A	3588	3	282	NSWDYRHPLSCLANFCIFSRDGGFT ILTKLVLNS*PRDPAASASQSVGITG VSTHGLASWN\FNKLKNSYTQVD*L GSQEWPLKVCLAKPRTAS
3326	8823	A	3589	1	714	
3327	8824	A	3590	1	726	MAEGETESPGPKKCGPYISSVTSQS VNLMIRGVVLFFIGVFLALVLNLLQI QRNVTLFPPDVIASIFSSAWWVPPC CGTASAVIGLLYPCIDRHLGEPHKF K\REWSSVMRCVAVFVGINHASAK VDFDNNIQLSLTLAALSIGLWWTFD RSRSGFGLGVGMLF\LATVVTHL*V YNGVYQYTSPDFLYV\RSWLP\CIFF AGGITMGNIGR\QLAMYECKVIAEK I/LIRNEEGKK\YLLYRKAR
3328	8825	A	3591	469	537	PGLARRAMASGRSHGWP*IPPLRST FQGGRTLDAAFTRINCHGKTYLFKG SQHWRFEDGVLDPDYPRNISDGFD GIPDNVDAGLALPAHIYSGRERVYF FKGKQYWEYQFQHQPNLEEREGSS LSAVFEHFAMMQRDSWEDIFELLF WGKTSAGTRQPQFINLDWHGEPWQ ADAAMAGRIYISG
3329	8826	A	3592	193	384	
3330	8827	A	3593	96	1635	ARSPAMAPLRPLLILALLAWVALA DQESCKGRCTEGFNVDKKCQRDEL CS\YYQSCCTDYTAECKPQVTRGDV FTMPEDEYTVYERLGEEKNNATVH EQVGGPSLTSDLQAQSKG\NPEQTP VLKPEEEAPAPEVGASKPEGIDSRPE TLHPG\RPQPPAEEELCSGKPFDAFT DLKNGSLFAFRGQYCYELDEKAVR PG\YPKLI\RDVWGIEGPI\DAAFT\RI NLFRGRPYLFKG*\QYW/RAFEDGV\ LGPWIYPRNISWTAFDGHSPGQTW D\AALGLPCPLAYSGRERV\YFFQRG KQYW/ESYQFPGTSPVQEECEGSSL\ SAVF\EHFAMM\QRDSW\EDIF\ELLF \WGAERSGWVTR\QPFHLAGEW\H GVPG\QVD\AAMG\GRILHLQGMAT RPLLWPKKK\RFRH\RNR\KGYRS\Q R\AHSRGR*PETPRRP\SRA\MWLSF VLPSEESNLGA\NNY\DDYRMD\WL VA\ATCEPIQECFFFSFGDKYYRVNL RTRRVDTVDPPYP\RSIAQYWLGCP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						APGHL
3331	8828	A	3594	44	166	
3332	8829	A	3595	3	1173	SSAPEAAKKPTPCHRCRGLVDKFN QGMVDTAKKNFGGGNTAWEEKTL SKYESSEIRLLEILEGLCESSDFECNQ MLEAQEEHLEAWWLQLKSEYPDLF EWFCVKTLKVCCV\PGT\YGPDCLA CQGGSQRP\CSGNGHCS\GDGSRQG DGSCRCHMGYQGPLC\IDCMDRLL QLRSRNETHSI\CTAVRTGLSDSYPP CCLSLGCWRGVGHAWIRGRNTHTQ PGYSSRVWIAAFSPACDESCKTCSG LTNRDCGECEVGWV\RTRAPCVDV EKCAAQT\PPCSAAQFCKNANGSYT CE\ECDSSCVGCTGEGPGNCKQCIS GYAREHGQ\CADVERVPH*PEKTLC EEKTKTCYNTPG\SY\VCVCPDGFEE T/RRCLCAAGRRLKPQKGESPTQLP LP
3333	8830	C	3596	1	300	MRSFGQLTLCPRNGTVTGKWRGSH VVGLLTTLNFGDGPDRNKTRTFQA TVLGSQMGLKGGAGSVWLQAAGL GLLPASLLWPSLLCHCYVLPPAPGV PLV*
3334	8831	A	3597	359	1229	MPQPPTLGQEMTGPSQPWTGKGGL PGP*QLRAKAQEVDSHLGRKKIKQ QNRSKSC
3335	8832	A	3598	2	311	VRWNSAAPLVTSRGAPASARPRGQ ALPGGSAPSAPHGQLPGRAQPAPVS GPPPTSGLCHFDPAAPWP\PGLGLG MLPPHPQDWPAQP*HPPGLGLFFEIF SAS
3336	8833	A	3599	1	426	
3337	8834	A	3600	18	738	
3338	8835	A	3601	65	425	RLPQPPGAAVGGSTRPCPSWKAVR VDLVVAPVSQFPFALLGWTGSKLF QRELRRFSRKEKGLWLNSHGLFD/R GAGKQQWQDS*VTEVLLLLQKTFF QAASEEDIFRHLGLEYLPPEQRNA
3339	8836	A	3602	3	233	FFFFFKTLQIPLLLSPPPPGPCRVQSL LPNPFPEKGA\PPFQTDERGQDFRLD PPLGSPSPRV*SLNCYVPVPPKEK
3340	8837	A	3603	7	510	THAPAPSPRAQAP*PLFIHCP*APRV TPPPPQPVKCVVPAEVI/SPPPPGPCR VQSLIPLTRFPEKGAYLLSRQMKRG QDFKAGIQPLGLSLPQPGSTGRGRV TAGD
3341	8838	C	3604	846	989	MKSYNGMREMGDQASRRKLIKNW TDSKFLDMENGEQKKITPRPGVKI*
3342	8839	A	3605	3	232	KSLLREGLESAMLVLKSLLPFSYFV SSMSSGNWSALHNHLGPEDTGTAS PYNRCS*RGRDHLGKRSSTRGTTLG PN
3343	8840	A	3606	303	400	
3344	8841	A	3607	3	404	LRQRLTVTQAGVQ*HRLSSLQPLPP RLKRFSCLSLPSSWDYRRVPPHMA NFLY/FLVETGFHHVGQAGLKLLISS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DLPALASQSAGTTGMRHRAQPKSF QLEQKWKTEPHKLIIYVVTLNKRM YKLKTYHIPYYF
3345	8842	A	3608	2838	3122	FFFFFFETKSCSVA\RLECSGTISAHC NLHLPGSSDSPASAS*AAGITGACH HTRLVFLYF**RRGFHHVSQAGLEL LT*VIHPPQPPKVLGLQA
3346	8843	A	3609	1	325	RLFFFFETVSHSVT\RLECT*AILAHC NLCFPRSSNSLASASQVAEITGACY YTQLIFVFSVETGFHHVGQAGLELL T*VIHPPPPPKVLGLQVSATVPGLII GTFSL
3347	8844	A	3610	3	398	GSLQPPPPRLK*FSCLSIPSSWDYKR LPPCPANFCIF\TELGFHQVGQAGLE LLTSGDPPASTSQTVGITGISHHAWP PEILSKGTMGKQMVNMLLLASSCR EMGHSAPAHLGQCLPMILPKDLAVI IINPV
3348	8845	A	3611	3	311	AQTGMQW\DLCSVKPPPPRFERFSC LSLLSC*DYKRTPTCPANFC/DFVVE TEFHHVGQAGLELLTSSDLPASASE NPQITGMNYCIWPEWYYYIHSLTNT IIK
3349	8846	A	3612	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRSL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCLSLPSSWDYRRPP PRLANFFVFSVETGF\TVSARMVSIS *PRDPPASASQSAGDTGVSQAPV
3350	8847	A	3613	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3351	8848	A	3614	335	477	TPASLKIPVE**NTLLAKMVSIS*PR DLPASASQSAGITGVSHRARC
3352	8849	A	3615	135	804	GIDTILTLNQN*SLKTRQ*FTLIIF/IFF FFLRWSLALSPRPDCGLQWRDLGSL QAPLPGFTPFSCLSLPSSWDYRCPPP RPANFFCNFFFSRDGGFTVLARMVS IS*PQ/CDPPTLASQRAG\ITGLSHCT RLFFF*WMESPSVTQAGIQWHDLGS LQPMPPQFR*FSWLSLPSSQDYRCM PPCQANF\CIFSRDEVSPC*PGWSGS PDLVIHLPWPPKVLGLHA
3353	8850	A	3616	3	285	HEIIVLRVRVSPCCPGWSA\TVD*SW FIAASYS*\VKRLSCLSLLRIWGCRQ VPPWLSFKLFWRQGLAVLPKLVSN SWPKMTLLPQPLRLLGLQE
3354	8851	A	3617	3	575	PSLRHASHEAGWQCPHLGQPLPGY TELRTELPQ*GDGYGRPGVSAASQR R/GLAGQCVEGRDWVEGKAG*CSG GHGGEGKGPLD*GALLPGPQNRS\S GAGDPC*AVESVGCQ*PGECHFQR DPPGSGAAPGAPPPAVP*LHRQPDA AAGGTAGPSLPHLPPPLPGLRVERS KPGGAAEEQGHPHLEHGPGD
3355	8852	A	3618	3	379	FFETESCSFTQAGVQWHDLGTL*SP PPGFK*FSLSLLSSWDYRRPPPPRTA/ NYIYIVFLVETGFPYVGQAGQKLLT

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SCNLPALVSQSARITGVSHCAQLCN FLLTVKHFKPLTLRLEARTPQSFLL
3356	8853	A	3622	1	214	ETESRSV/SQAGVQWRDLGSL*PPPP PGFQRFSCLSLPSSWDYRRAPPLPH NF\CIFSRDGVSPCWPGWSQIS
3357	8854	A	3623	2	309	WCVFFETETHSAAQAGVQWCNLSS LQPPPPGVKQFSCLSLPSSWDYRCA SPCLASFCIFSRA*GFTMLTCLELLT SGNPPTSASQSAGIQG\VSHHTWPSI F
3358	8855	A	3624	1	294	FFFFFFLRQGLTLSARLECSGMISAH CSLDLPG\SGDPPTSAS*VAGTTGTC HHAWLIFLFLVETGFHHVAQAGTLS KHRNHIQPVEQVRATCSKDGQ
3359	8856	A	3625	23	282	ASTGKPLSPQVQSES/CLALQLP*RS WN*TRVMSTTPWPNFFGIFVEMGF RHIGQAGLELLTSSNPPILASQSAGI TGLSHRVQPTSS
3360	8857	A	3626	37	289	QWHDLGSLQPLPPGF\RRLSCLSLTS SWDCR/QPALRPANFFCIFK*RWGF TVLAQDGLDLLTSSDLPASAS*SAGI TGVSHRAWA
3361	8858	A	3627	70	362	KLHFKAIEGISSLGEQMKPSMWML LCPQIKIKLTLPIQIKQAKTCRQIPKV QGSQ*KNVGPSSFPVPW/EHGSGMI EAPWALNPYLGLGPVQILETQK
3362	8859	A	3628	60	303	KLKNHHHHHQQQQQKQQQQQKK QMDPRVSFSFFKKKKSSTPKPSQ*FP *SSRNS/HPR*ISESDTLRPTEAIPIGL KMKLPL
3363	8860	C	3629	193	285	MLLVSYPRNSNRCQIQYHEAFCPIIF LRVL*
3364	8861	A	3630	159	483	DPTSFGHGYLVFPTPCFKGFYFF*DR VSFCCSGML/IGSLQAQPSGFKPKPS SHLRLLSSEDCRHTPPRLANLFFYFF L*RWDLTMLPRLVSNS*AQVILPSW PPIMLG
3365	8862	A	3631	6	244	DRVLLVTQAGVQWHDLGSLKPPPP GFK*VSCLSLPSSWNYRRLPPRP\AN F*FLVETGFLHVCQAGLKLPTSGDP PASA
3366	8863	A	3632	2	262	NDLGSLK\PPPPGFK*VSCLSLP/RVS WNYRRLPPRPSLIFVFLVETGFL\HV CQAGLKLPTSGDPPPSASQSTW\ITG VNHRARPQIGF
3367	8864	A	3633	1	1149	
3368	8865	A	3634	280	602	TDFFFFFFLRWSFTLVAQAGV*LHD PE*LQPPPPGFKRFSCLSLPSSWDYR HPPPWPANF*FLVETGFHHVGQAG LELLTSGDPPASASQSVGITGVSHR ARPELNF
3369	8866	A	3635	3	679	SLHQSGRSNPTCCFPSSKGTGTNGH PTPSQPSPPGTRDGPLFPFPHSASTPP PTGASQPLTGTRGPPSPVEPVSHAC ASL*FSEGLRSEHPAVACGKTLQSP TGSKPEACSGEQGNCVLAEIVVLGT QDPSAH*GGAGARGGGALWVTEG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VKGPGPVSGQCRKSQPHACGEIPCR APPTMGTSGPL\GLPKLCPHFHCSRG ASPAPSNSPFCFWSPTSGGPNPFPC
3370	8867	A	3636	1	334	EMESRSVAQAGVQWHDLGSLQPLP PGFKRFSCLSLPSSWDYMRA/P/PRP G*FFVFLVEMGFHLVGQAGLKLLTS /S/DLPTSASQSAGITGMSHRTRPNSL LVIQSGRFNTKITR
3371	8868	A	3637	2	309	FFFFETRSRFVAQAGV*WHAYGSPQ PRPPGPKPSSQLSLPS*DYRHTLLCL ANF\DFLVETGFYHVAQTGLELLSV RDPPALASQSAGIAGVSHRARPGCI F
3372	8869	A	3640	19	458	KHLFYSSNLYFRSTFRHTRRRSPCEP SLALR/WCVLEPGSSRV**RLHPNTV GFQDASAKPRERTTSFHAFAFNF*K QYIFQC*LPPLTWLEIFSPFSRETKST KRCRLQDPGPSHFWRVVLCGLLWG QDRAPSWAPLQMQLCHCLYL
3373	8870	A	3641	1	322	FLRRSLALVTQARVQWHDPGSLQP SPSGFKRFSCLSPPSTRDYRHPPPRL ANFF/VFFLYL**GFATLAWLVLNSH L/CDPPASASQSARTTGASHHAQPP VSFFKTRI
3374	8871	A	3642	333	438	
3375	8872	A	3643	391	492	
3376	8873	A	3644	598	699	
3377	8874	C	3645	176	319	MCSAQPAFSVDIIKSRHLGILGFEYK PRILCQKHMLRLLHSFQNFQR*
3378	8875	A	3646	2	50	QLLGTTGMHHYA*LIF
3379	8876	A	3647	3147	3308	FFKKNLCASAHYY/TWCVPLPFFFF LRQGL/NSIGQAGVQWCNHSSLQPC PPQDLE
3380	8877	A	3648	1554	3041	GTRERRAPDPCAGKCRNHVAGGRL KLSLHLSLPSSWDHRHAPL/PHD*FF KYLRR/RSPCVTQAGLKLLGSSDPPI LASQSIGITDMSHCT/WPSSPTPCHF LRDSFAPSPRPGMQ*CDHSSL*PQTL GLKQFSHQPPFYFFVQMG\FAMLPK LVLNSWPQ/DNPSALAPQSAGIVGM SCCAQPPCFNINSHS*IQE
3381	8878	A	3649	280	444	
3382	8879	C	3650	135	377	MAGSWGAGQVQWLMSVIPILWEA KMGGSLEPRSLRPAWVTQGDPVSN RLFHSSASVLWLQATLGTIPKSLEYI TLAFRAK*
3383	8880	A	3651	1791	6596	CPKDTQILIFQKNNFSIRRFTQHLAD FLKEFCLTFKKKGRSQLL*FCCFVYI IF*KKFVCFCSLLHWCVPLPFFFFLR Q/RSHSIGQAGVQWCNHSSLQPCPP RLK\HPCTSASQVAGTTGMHHYA*L IF*IFETGSPCVTQAGLK/PPGLK*SS HLGLPEYWDYRHEPLHLPSSPTPCH FLRDSFAPSPRPGMQ*CDHSSL*PQT LGLKQFSHQPPFYFFVQMGSCYVA QAGLK/PPGLKQSFCLGPPKCWDCG HELLCPASMF*YQHPHMYTLKTTV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TFSTQNYIRYSLNCRKIKTIPKSDCR VDFFLQNT
3384	8881	A	3652	3	332	ETESHSVAQDGVQWRHLSSLQPPLL GFK*FSCLSLPSSWDYSCPSPT/P*LI CFFFFFLIEPGFHHFGLAGLELQTSG DLPASAFQDAGITGMSH*TRPELLS LDHTPFT
3385	8882	A	3653	3	272	FETESHS/VSPRLECSGVIFAHCSFCL PGSSDSPASAS*VSGMIGTRNHAQLI FVFLVEVRFHHVGQAGLELLA*VI HPPQPPKVLGLHV
3386	8883	A	3654	1	272	ETGSRSIT\RLECSGAITAHCSLDLPG RSNPPTSAS*/RIAGASGECRHTQL/I* KFIFFVNTGCRYVVQAGLKLLASGA KQSSCLGLSKCWD
3387	8884	A	3655	249	906	RIHFPRVSGPSQSNPKFAVASRGFFS LSLSSAQPDPLPPPLGEALALSLHPV PRRSTETVAGDSSELQLGLRSPQQP LAGLAFLARLFLLFPPP*RCKSKPN* NDRRRSSVDSQIHLVGRESAHPLAG LRVCVSLPLLARCFGQVLQGVPGL WIPSPGGS/AGVSGRRREERHMGVV VMRVRVEARVSS*ESKI/SRALR*ST HLGLPKCWDYRREPPCPAH
3388	8885	A	3656	1	514	FFFFSRSL/NSVIQAGAQWRDLGSLQ P/LLPPGLKQFSCLSLLSSWDYRCPP PRLANFYIF/M*RRGFTILARLVLNS* TQ/CDPPTSASQSAGITGVSHPTQ/LL FSF/CLKESGSSLMVSATLRFHK*RH SGPSRAALSSSP*LEPRKLKFGTASL QNKWAMQQTRQHWAQRGSKPM
3389	8886	A	3657	2	307	FFFFFFFETESYSVTQAGVQWHDLGL LQPLPPGLKQFSSLSLPE*L/DVTGSP PPCPVNFCTFGKGLGFTMVGQAGS GTSDLKVICPPGLPKVLGITGCEPRR L
3390	8887	A	3658	79	91	NTFW*RRGFTVLARMVLIS*PHDLM TC/PASASQSARITGMSHCARLVLYF SRDGVSLCWPGWSQTADLR*STCL GLPKCWDYRYEPPCPASLHHFLIYA TSIIKYL
3391	8888	A	3659	162	493	DGSSPPVAQAGVQWRDLGSL\QAPP PGFTPFSCLSLS\RSWDYRRPPPRPA NF/SCIFIVETGFHRVSQDGLDLLTS* S/VPASASQSAGITGVSHRARPRSCIS FDSTVTLAQ
3392	8889	A	3660	3	251	GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDLGSLQPPPPRFKRFSCLI LPSSWDYRH
3393	8890	A	3661	3	251	GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDLGSLQPPPPRFKRFSCLI LPSSWDYRH
3394	8891	A	3662	17	287	KYHRIQCPNSG\CEAVYSSVSGLKA HLGSCTLGNFVAGKYKCLLCQKEF VSESGVKYHINSVHAEVRLL*SCGP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DM*ATREVDFVPIVMD
3395	8892	A	3663	3	567	DRKLKYTRPGLPTFSQEVLHKWKT DIKKYHRIQCPNQGCEAVYSSVSGL KAHLGSCTLGNFVAGKYKCLLCQK EFVSESGVKYHINSVHAEDWFVVN PTTTKSFEKLMKIKQPAARRRKAEA AAQEQKVSKKGGSSLGIELPETEPS LRVGKDQRRNNE\DW*CQPPCKEP/ GAGASASTVPESKAPKD
3396	8893	A	3664	1	184	SSRDILLCTDIASRGLDSTGVELVVN YDFPPTLQD\ELAARRRRSLPGLASS VKEPLPQAT
3397	8894	A	3665	2	1748	HEARTKGNMALSAARLRLLFPFVN SVCFLAP\RRGL\TVRSPDE\PLP\VVR IPVASTSGKLEQRQ\SRRRNLPEGRC LVRPGPLLVSARRPELN\RPARLTLG RWERAPLASQGWKSRRARRDHFS\I ERAQQEAPAVRKLSSKGSFADLGA WKPRVLHALQE\AAPEVVQ\PTTVQ SSTIPSLLRGRHVVCAAETGSGKTLS YLLPLLQRLLGQPSLDSLPIPAPRGL VLVPSRELAQQVRAVAQPLGRSLG LLVRDLEGGHGMRRIRLQLSRQPSA DVLVATPGALWKALKSRLISLEQLS FLVLDEADTLLDESFLELVDYILEK KDLAVFLYHLRLEAEVEVVEMLGP HGQPCPQHNSDISAYTYERTLMME QRSQMLRQMRLTKTEREREAQLVK DRHSALRLESLYSDEEDESAVGAD KIQMTWTRDKYMTETWDPSHAPD NFRELVHIKPDQSNVRRMHTAVKL NEVIVTRSHDARLVLLNMPGPPRNS WCTTSSRTEKRQWNCPAVRTEKNA QTRQTIIAETKTQKKDTEPRIPEADL AVQYDNHYTNTKYCLCQMLREQL ESPQGRLLHAAQSSREIW
3398	8895	A	3666	1	1704	MALTRPVRLFSLVTRLLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLPRPVLVRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLEPRVLHALQEAAPEV VQPTTVQSSTIPSLLRGRHVVCAAE TGSGKTLSYLLPLLQRLLG\HPSLDS LPIPAPRGLVLVPSREFF\QHLRAVA QPLGRSLGLLVRDL\EGGHGMRRIR LQLSRQPSADVLV\ATPG\ALW\KAL KSRLISL\EELSF\LVLDEG\DTLLG*K ASWELV\DYIL\EKSHI\AEGPADLED PFNPKAQLVLVGATFPE\GVGQLLN KVASPDAVTTITSSKLHCIMPHVKQ TFLRLKGADKVAEL\VHIL\KHR\SR AEKGLGPSGTGF\VFCNSSSTVNWL GYILDDHKIQHLRLQGQMPALMRV GIF\QSFQKSSRDILL\CTDIAS\RGL\D STGV\ELVVNY\DFPPTLARLTFHRA GESGPVWGAEGPG\TVI\SFVTHPW DVNPWFKKD*SLAARPKEEVLPGL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AIPR*KKPFAPQSNPDFEQNLIKM
3399	8896	A	3667	2	222	RWSLTLFQAGMQW\PNLSSLQPPPP RFKQF*CLSLPSSWDYWYTPPRLAN FCIFSRDGVSPCWSGWSRTPDLR
3400	8897	A	3668	1	29	
3401	8898	A	3669	2	206	VTQAGVQWLALSSLQPLPPG/LK*F YCLSLPSSWEYRHTPPHPTKFCIFFL VEGVSPYWPGWSQTPGLR
3402	8899	A	3670	3	139	TSHMWWCRHVVSATREAEVGEPL EPRQSRLQ*AMTAP\CTPAWATK
3403	8900	A	3671	86	384	
3404	8901	A	3672	3	746	RQEEGLPPVVDAIDDASVEEDLAVA VAGGRLEEVSFLQPYPARRRRALLR ASGVRRIDREEKRELQALRQSREDC GCHCDRICDPETCSCSLAGIKCQMD HTAFPCGCCREGCENPMGRVE\FNQ ARVQTHFIHTLTRLQLEQEAESF/QG AGGPCPGQPTQPW*GGPGPYFPTGQ APHEQ*AGRQQLQQRHD\YSSTASS SASGTSEAPDCPTHPGLPGPGFQPG VDDDSLARILSFSDSDFGGEEEED
3405	8902	A	3673	72	332	LPALETPRAQSKCSPPQPSWVSRDY RCVPTHALANF*IFGEMGS/LLCCPR LISNS\WPQGILPPPPPKVLGLQGSYS AKITTGFFLK
3406	8903	A	3674	33	396	RVWYLHRVTGRPASCLREVGPGDS LETASLREIWRSRRCRAT/ECSQQRL NHRLARQREHEARLRQQREQNSRY FTDV*HL\RSKQAEWSSKTYYQRSM HAYHREKMKEEKRRSLWARLEKL M
3407	8904	A	3675	217	935	QRQREKEDQIRQQWEQNSRYFRMS DICSSKQAEWSSKTSYQRSMHAYQ REKMKEEKRRSLEARREKLRQLMQ EEQDLLARELEELR/REHELAGKKN PGAAREAEISQRRAEETDC*TTFVR TLEKEQPETSRDGAGPSPEACRKLL GNAE/MKKKKQQEASAEQGNKRYE NEYERARREALERMKAEEERRQLE DKLQAEALLQQMEELKLKEVEVGT SPSQP*PPPQLLVSMRWALERLP
3408	8905	A	3676	1	382	EMEPCFVS*TGV*WHDLSSLQPPLP KFKRFSCLKIPE\SWDYRRTP/PMP/V LTGFHHVDQAGFELLTSSDPPTSAS QSVGITGMGDHTWPTLHTLTKPCE VDENAVMRELKLTGQGPLRKWQF EHLNPA
3409	8906	A	3677	1	2456	MPTYPKLEKTDQSTSYTKFNDLSPD SSRERYTSLEIKSVCYTALPEQGQK QLQLWYNCVKTQCKTTQECSLKWI FTMNETSDREDGLPKGHHVTDSEN DEPLNLNASDSESEELHRQKDSDSE SEERAEPPASDSENEDVNQHGSDSE SEETRKLPGSDSENEELLNGHASDS ENEDVGKHPASDSEIEELQKSPASD SETEDALKPQISDSESEEPPRHQASD SENEEPPKPRMSDSESEELPKPQVSD

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SESEEPPRHQASDSENEELPKPRISD SESEDPPRHQASDSENEELPKPRISD SESEDPPRNQASDSENEELPKPRVS DSESEGPQKGPASDSETEDASRHKQ KPESDDDSDRENKGEDTEMQNDSF HSDSHMDRKKFHSSDSEEEEHKKQ KMDSDEDEKEGEEEKVAKRKAAV LSDSEDEEKASAKKSRVVSDADDS DSDAVSDKSGK\KRRTIASDSEEEA GKELSDKKNEEKDLFGSDSESGNEE ENLIAD\NLENLVMKRK*NLQVLTK KIWEEEKGETQVKEAEDSDSDDNIK RGKHMDFLSDFEMMLQRKKSMSG KRRRNRDGGTFISDADDVVSAMIV KMNEAAEDLKETFIDSGVMSAIKE WLSPLPDRSLPALKIREG\VLKILQE LPSVSQETLKHSGIGR\AVMYLYKH PKESRSNKDMAGKLINEWSRPIFGL TSNYKGMTREEREQRDLEQMPQRR RMNS/DLVVRHPERDLEKVLTGEEK ALRPGDPGF\VPRARVPMPSNKDYV VRPKWNVEMESSRPGILKKGLSRLE KHKRRFAEQKRLSKVHRAVKFSIEG NRMPL
3410	8907	A	3678	1	564	TLKQVGLTEHVMYLYNDPKESRSN KDMAGKLINEWSRPIFGLTSNYKG MTREEREQRDLEQMPQRRRN\DST GGQTPRRDLEKVLTGKEKALRPGD SLNLV/PRARVPMPSNKDYGVRPK MKCGNGVIQVSGDPPQKGIQSDWI NQMRKFHRY*GKKADLAHAVENP AIEGNKMPIGDPCPGMCPPILLL
3411	8908	A	3679	63	361	
3412	8909	A	3680	151	384	
3413	8910	B	3681	385	479	MAGAFRRRFASEVRAQGLESLLEH GLRCAGSLRGGQSLPTTMWSPVKV GFE*
3414	8911	A	3682	3	698	VFFFFFSGCTRGPLFESDFHRAPHRC GQGLAAP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGQAA\PPALVP GEGPSWDSDPRGHRCSQATLPRVL AGPLQP*LS*LSL*DPPELRSL*PPL* LRLL**SLEPP*PPLLDSNRFPP*PRSP PPLENPRPRPRPPRKKPRPPAEPPRY PTESVSDDLPAWSTRISVHLQTSHS WPSWASLASSMFFKVTKPNSRELW SS
3415	8912	A	3683	138	550	FCCCFTSSEHSLLAYGSCSPRRTEVL CAQQNPSETQAAPLAS\YMWK*PC NSRLKGPGPGLGEGWPES\RMTSGV TVPGGTSPGTRAGGS\PCPGGLSPEA LRQ*GAGSGPRVSPGA/PGCGAPAA YGAASPCPQRCGAL
3416	8913	A	3684	2	555	FFFFFFLGAHVALYSNPTFTGLHIVV GKDWPPP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGASGCLQLLF QGEVPPGDS*PQRSSLALRPPFPRVL GPGPFQP\AKAKQRYSQRPPQGSQL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						APP/GPPRKQPQPLRKVSG*SGGCDL RLRHRPACPGRVCTLAQLEPATRM GWSYVGQCGL
3417	8914	B	3685	95	371	MASDEGKLFVGGLSFDTNEQSLEQ VFSKYGQISEVVVVKDRETQRSRGF GFVTFENIDDAKDAMMAMNGKSV DGRQIRVDQAGKSSDNPIPWX*
3418	8915	A	3686	314	1055	SKCFHLHQVWKQKGEEYRVTGYG GWSWISKTHVYRFVPKLHGNTNVN YRKSLEGTKNNMDENMDESDKRK CSRSPKKIKIEPDSEKDEVKGSDAA KGADQNEMDISKITEKKDQDVKEL LDSDSDKPCKERTNGSRR*HENRVT CKLSGEFSSRCGQC**GFSSKD*LQK ENKIIQTRWTS*KEN*TVYTGRKTA TRKNQVGGWN*GYRKD\STNSSKN LSESPVITKAKEGCQSDSDETRTEPK CK
3419	8916	A	3687	11	345	DSLTVAQSGVQWHNLISLQPLPPGV K*LFCLSLPSS*DYRRAPPHPANFS\F LVEMGFYHVGQAGLELLISSDLTSL ASQSAGITSVSHWAWPENVYLNLQ QTEKSLMVSG
3420	8917	A	3688	1	521	NPTKSCMLEG*NPHVHCK\REGAQA ITGMPI*KATKYLKYFLLQKLCVPF QS/YESGVGRCTQDRHWGWTHHQ WPRKGTEICLQVQSYAELKGIDVDS LVIEHIQ/V/NKAPIMYHLTYRTHGQ MNP/YHKLPCHIQMMLSEKKHLVP KAEKEDARKKKIPQKKHKLKRQTN SAKRKCK
3421	8918	A	3689	1	281	ETGSHSDAQAGVQWHDLGPMQPLP PGFKRFSHLSLLSSWDYRHAP/PRPG LFL*RWGFHQVGQVDLELLNSSDPP ASTSQSAGITSASHRAWPN
3422	8919	A	3690	3	314	HAEHEITELTATFTKFDRDGNRILDE KEQEKMRQDLEEER\LTRRVLQLET VLERVVAQIDALSSKLEMLEKKGV SLSLFTSFNIRAFKSLFSHYSSVTPIN YL
3423	8920	A	3691	61	400	LVTGIWSATCLWVLLLLLFEKGCPS VQPRLQCS\NVITACCSLNL\RGSND PPTSASRVPGDHRCCHYTWANFLIF LWEMRSHCVGFRLGLGTPVLKLQT ILQPQPPKVLGLQA
3424	8921	A	3692	33	436	REQEL/CKGKQKDGTSFGEYGGWY KACKVDSPTVTTTLKNLGALYRRQ GKFEAAETLEEAAMRSRKQGLDNV HKQRVAEVLNDPENMEKRRSRESL NVDVVKYESGPDGGEEGVSGRASF CGKRQQQQWPGRRHR
3425	8922	A	3693	37	355	NSEYGGWYKACKVDSPTVTTTL\K NLGALYRRQGKFEAAETLEEAAMR SRKQGLDNVHKQRVAEVLNDPEN MEKRRSRESLNVDVVKYESGPDGG EEDGTGSLKRS
3426	8923	A	3694	229	2000	QRERARPSGARRMYDTMSTMVYIK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EDKLEKLTQDEIISKTKQVIQGLEAL KNEHNSILQSLLETLKCLKKDDESN LVEEKSNMIRKSLEMLELGLSEAQV MMALSNHLNAVESEKQKLRAQVR RLCQENQWLRDELANTQQKLQKSE QSVAQLEEEKKHLEFMNQLKKYDD DISPSEDKDTDSTKEPLDDLFPNDED DPGQGIQQQHSSAAAAAQQGGYEI PARLRTLHNLVIQYASQGRYEVAVP LCKQALEDLEKTSGHDHPDVATML NILALVYRDQNKYKDAANLLNDAL AIREKTLGKDHPAVAATLNNLAVL YGKRGKYKEAEPLCKRALEIREKV LGKDHPDVAKQLNNLALLCQNQG KYEEVEYYYQ\RFLEIFQTKLGPDDP NVGKTKNNLASCYLKQGKFKQAET LYKEILTRAHEREFGSVDDE\NKPI\ WMHAEEREECKGQQKDGTSF\GEY GG\WYK\ACTVDSPTVTTTLINLGAL YRRQGKFEAAETLEEAAMRSRKQG LDNVHKQ\RVAEVLN*PLRTLEKPQ EPVESL\NV\DVVKYESGPDG\GEEV SMSVEWNGGVSGRASFCGKRQQQ QWPGRRHR
3427	8924	A	3695	1	314	KVDSPTVTTTLKNLGALYRRQGKF EAAETLE\EAAMRSRKQGLDNFTKQ RLPEVLNDP\ENMEKRRSRESL\NVD VV\KYESGPDGGEEVSMSVKWNGM RKMKLGAG
3428	8925	A	3696	2	450	VNKAGGLIYQLDSYAP/RAEAEKTF SYPLDLLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTADGK EVLEYLGNPANYPVSIRFGRPRLTS NEKLMLASMFHS\IKFVVLADP\RQ AGIDSLLRKIYEIYSDFALKNPFYSL EMP
3429	8926	A	3697	2	823	FGTRGKAAMAIFSVYVVNKAGGLI YQLDSYAPRAEAEKTFSYPLDLLLK LHDERVLVAFGQRDGIRVGHAVLA INGMDVNGRYTADGKEVLEYLGNP ANYPVSIRFGRPRL\TSNEKLMLAS MFHSLFAIG\SQLSPE\QGSSG\IGCLE TDPFQFH\CSRTLTGIKF\VVLADPR\ QAGIDSLLRKDFMEILLQTLPLKNPI PIPLEMP\IRCEPL*PQNPEA*SLEVA\ EKAG\TFGPRVHRLNPVMGPPQNPE SSLQQEYCLLTLPVEIPAALVSAP
3430	8927	A	3698	165	354	ENFGGKITNFAKLFGYILPYSHYFW CLEKNRNR/SLTLLPRLVSNSWAQA FLLLWPPKVLRLQA
3431	8928	A	3699	3	166	SETGFCHVAQAGLELLVSRSPPASV SQS\TGISHQARPSISYFYDHSAPITH TDH
3432	8929	A	3700	1	421	ETKSHSVTKTEVEWRDPSSLQPLSP GFKQFSCRSLPN\SWDYR/PSPANFV FLVETGFYLVGQAGLELLTSNDPPA SASQSAGITGVSHCAQPRITNSLTTA SFIQPRKHSEFPVMTCPPSSNATESK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VGGRGPHGAIARLM
3433	8930	A	3701	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADML\ VSFSGYSSAPKNQEQ
3434	8931	A	3702	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADML\ VSFSGYSSAPKNQEQ
3435	8932	C	3703	282	445	MISAHCNLLPPEAGELLEPGGRRFS EPLHSSLMTEQDSVSKINKNNKTSIS NPE*
3436	8933	A	3704	170	607	WPSG*FQR*SMRLLKYKIHLNVSRR PQLAPGKELYFSF*LLFYFYFYFIIIIII FEMESHSVT\RLECSGTISAHCNLHL PGSSDSP\ASASPVAGTLIDACHHTW \LIFYNF*VEMGFHHVGQAGLKLLT\ *VTHPPRPSKVLGLQA
3437	8934	A	3705	3	231	FETESLFPRLECSGTISAHCNLRLSG SSNFWLIFCI\LVEMGFHHVGQTSLE LLTSSHPPTSAFQSARITGVSHRTW
3438	8935	A	3706	4	144	
3439	8936	A	3707	333	416	FTGLPCLFSPQNNVSLLQSCID\LFK NN
3440	8937	A	3708	1	1219	MAAVPELLQQQEEDRSKLRSVSVD LNVDPSLQIDIPDALSERDKVKFTV HTKTTLPTFQSPEFSVTRQHEDFVW LHDTLIETTDYAGLIIPPAPTKPDFD GPREKMQKLGEGEGSMTKEEFAK MKQELEAEYLAVFKKTVSSHEVFL QRLSSHPVLSKDRNFHVFLEYDQDL SVRRKNTKEMFGGFFKSVVKSADE VLFTGVKEVDDFFEQEKNFLINYYN RIKDSCVKADKMTRSHKNVADDYI HTAACLHSLALEEPTVIIKYLLKVA ELFEKLRKVEGRVSSDEDLKLTELL RYY\MLN\IEAAKDLLYRRTQS/ALI DYENSNKALDKARLKSKDVKLAEA H\QQECC\QKFEQLS\ESAKEELINFK \RKRVA\AFRKNLIEMSELEIKHARN NVSLLQSCIDLFEE
3441	8938	A	3709	527	724	TMKIGLGFSLVSINIFSFPVELINFKR KRVAAFRKN\LIEMSELEIKHA\RNN VSLLQSCIDLVKNN
3442	8939	A	3710	1	1220	QEGGSAGSAGSGADGTGLRQSLAG HVGRPGRGQWGQRGSGDLPGHRPP PARSEHRCVAEG/NLSLYVFGGYNP DYDESGGPDNEDYPLFRELW\RYHF ATGVW\HQMGTDG\YMPR\ELASMS LVLHGNNLLVFGDTGIPFGESNGND VHVCNVKYKRWALLSCRGKKPSRI YGQAMAIINGSLYVFGGTTGYIYST DLHKLDLNTREWTQLKPNNLSCDL PEERYRHEIAHDGQRIYILGDGTSW TAYSLNKIHAYNLET\NAWEEIATK PHEKIGFPAARRCHSCVQIKNDVFIC GGYNGEVILGDIWKLNLQTFQWVK LPATMPEPVYFHCAAVTTA\GCMYI HG\GVVNIH\ENKRTG\SLFKIW\LVV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PSLLELAW\EKLLGAFP\NLANL\SRT QLLH\LGFTQGLIERLK
3443	8940	A	3711	2	266	FLMESRSVTRLECSSTITAHCNLCLP VSSDSAVSASQVAGTTGMRHHAQL IFVFLVETGFHHVGQDGLHLL/NIVI HLPRPPKVLGLQA
3444	8941	A	3712	1	453	FKRAMDLVQEEFLQRLDFSQHSWL PARALVEEALAQRFQVDPSGEIVEL AKGACPWKEHLYHLESGLSPPVAIF FVIYTDQ/RWTVANIAGCPLPEPWR GLRDEALDQVSGIPGCIFVHASGFIG GHRTREGALSMARATLAQRSFLPQI S
3445	8942	A	3713	20	891	RWNSRYDHHQRSFTETMSSLSPGK PWQTKLSSAGLIYLHFGAQ\VLAQL LGTSEEDSMVGTLYDKMYENFVEE VDAV\DNGISQWAEGEPRYALTTTL SARVARLNPTW\NHPDQDTEAGFK RAMDLVQKEVSCRD*IFYQHSWLP ARGLGGKSHLPQRIPRWNPSGK\IVE LAKRCHVPWKEHLLPPGNLGLSPS KWPIFFVIYTD/SRL/EQWRIQCVAQ/ VSPTHSQSRAA\LPEPWRGLRGTRP WT*FSGIPGCIFVHASGFI/SAVNATR EGALSMARATLAQRLIPPTNLLV
3446	8943	A	3714	176	450	
3447	8944	A	3715	1	472	
3448	8945	A	3716	418	1354	AAARRATCLGCRSCSGATARRASS WRTAPRVHSVAWKL\DGRRLASGS FDKTASRLLAWRRTRFGQKKTIIGG HGG*C/VTSFCWHPSNPEPICYGV/Y GDKTIRIWECEDYKNALPLVN\IKGE NINICWSPDWQTIAVGNKDDVVTFI *CQDTPFQSRRAVQVPRSTKSPWNH DHNMFLLT\NGNGCINILSYPELKA\ VQSINAHP\SN\CICNQV*PHGESTLP QASCKMLLVSLWDVG*VSVCFGAF SRLDWAC*EPFSFSHDGKMLASASE DHFIDIAEVETGDKLW\EVQCESPT\ SQVAWAPQKASAGHLPR
3449	8946	A	3717	1	296	LWDV/EELVCVGAFRLDWP/VRTSV SAHDGKMLASASEDHFIDIAEVKTG DKLWEVQCESPTFTVAWHPKRPLL AFACDDQKTANMTSSREAGTVKPV GAS
3450	8947	A	3718	2	276	RSTFALVAPAGVQWHDNRSLQPLL PRFKQLSCLSLLSSWDYRCPPPSPA NF/SLFLVETGFRHAGQAGLQLLTS GDLPTSASKSAGITGMGLQ
3451	8948	A	3719	3	613	GLRALRRGQGLPGL*CCSRPQPSPR AQGHPSMGGPMQRVTPPRGMASV GPQSYGGGMRPPPNSLAGPGLPAM NMGPGVRGPWASPSGNSIPYSSSSP GSYTGPPGGGGPPGTPIMPSPGDST NSSENMYTIMNPIGQGAGRANFPLG PGPEGPMAAMSAMEPHHVNGSLGS GDMDGLPKSSPGAVAGLSNAPGTP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RDDGEMAA
3452	8949	B	3720	134	471	MYAKGGKGSAVPSDSQAREKLALY VYEYLLHIGAQKSAQTFLSEIRWEK NIMPSPGDSTNSSENMYTIMNPIGQ GAGRANFPLGPGPEGPMAAMSAME PHHVNGSLGSGDMDG*
3453	8950	B	3721	223	692	MEPSPRAQGHPSMGGXMQRVTPPR GMASVGPQSYGGGMRPPPNSLAGP GLPAMNMGPGVRGPWASPSGNSIP YSSSSPGSYTGPPGGGGPPGTPIMPS PGDSTNSSENMYTIMNPIGQGAGRA NFPLGPGPEGPMAAMSAMEPHHVN GSLGSGDMDG*
3454	8951	B	3722	228	292	XLARDDHERVMGRQPRASLRA*
3455	8952	A	3723	1	1753	MYAKGGKGSAVPSDSQARENLSAF QAATELTSLDRLALYVYEYLLHIGA QKSAQTFLSEIRWEKNITLGEPPGFL HSWWWYGLGCCGVFWDLYCAAP DRREACEHSGEAKAFQDYETPERP AHRHGNAGRAGSSSGMIDVGGSSD PQILRPTTPVCSLTNASSLSHGAGHL QRGGGTPQSAAAAPSPVMGSMAPG DTMAAGSMAAGFFQGPPGSQPSPH NPNAPMMGPHGQPFMSPRFPGGPR PTLRD\GSQPPAGPPWVPSPSSPG\A MEPSPRAQGHPEHGRPNARGVTPP RG/MGPAWGPRAYGGGMRPPPNSL TRPRACLPMNMGPRKFVGPWAQPP VEYSIP\YSSSSPGSYTG\PPGGGGPP GTP\IMPSPGDS\TNSSENMYTIMNPI GQGADRANFP\LGPGPEGPMAAY\G \GMEPHHVNGSLGSGDMDG\LPREF PQAPVAGLSNAPG\TPRDDGEMAA AGTFHAPSSQSE\NYSP\GMTMSRV NWAAAPGALCGPRLLPRRPCLRAK GLKVTPSGTLDSLANQGLPMLGGP TRKTLTILLKTQGPRETFFSVWTLPA ICILVPERKALWGGPSSPGRQGGGA H
3456	8953	A	3725	65	210	ATRAGLIFDDSFEHDVWQDASSFRL IFIVDGWHPELTPQQRRS\LPAI
3457	8954	A	3726	2548	3800	NSLILLFFFFFRQRSLTLECSGVISAH HNLHLPSSSNS/P/ASAS*VAGITGM HRHAWPICIFLVETGFRHVGQAGLE LLTSGDPPAPTSQSM*ATTSGLILLL SKILFPFHSTKVFK*SCPS*KILKEEN CSVINEWFNSESSYTSKEKNNLVPN AC*EI\TM*VATNCDFT/SLL*RSENY PKLFHNNETTSQKIHLKIKISRPATS GQW\ILFSLVWWRARKG*GILMIHN GILY*TIC*IKLHRLP*GMDYPNQPD/ MKSGWDKRMSHTL*F*GKEIVFDF QNQQNKLSTLYLSVQE**HEEFFFR DLKYNKPGSTIKSLVSF/HSLTLFFFF FFEARSHSASQAGVQWGNIGSLQPA PPGLKRSSYLSLLSSWDYRRVPPHP ANFCIFCR/GWGFGVSPCCPGSSGTP VLKWRAHLSLPNC

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3458	8955	A	3727	2	217	SSPSPPHPPASPPSSPSP\PASPPPPSLP LPSPDFPPLSPCSSLSPFSSFSPPPSPP SPPFSRGPSPSDNFH
3459	8956	A	3728	25	396	ISGRSTFSLFSRQGLSALSPRLE\CSV AISAHCNLRLPGSSN\GTTGA*HHTR LILYF/LAEMGFHHVGQAGFEVLTS SNPPASASTSARITGMSNRT\GHLFN FHP*MCYKYRCGSLAGRGGSRW
3460	8957	A	3729	80	460	YISLNVTTHLIFFFFFLRQGL\CSVTQ AGV\QWCNLGSLQPLPPRFK\NWDY RCVTPHLANFVFLVEMGF/LPASAS QSAGITGVSHCTQLGVFICICYGSSH GVRQSWHQFCSSKLLVKSGRVGVG LLG
3461	8958	A	3730	1	316	FFFFFETESHSIVQAGVQWRDLSSL QPPPPRFKRFSSLSLPSSWDYRHVPP RPA\NFAFLVEMGFHHVGQAGLELL TPGDPPSSASQSAGMTGVTHCAWP RCLMF
3462	8959	A	3731	3	1717	RPQTLKGHQEKIRQRQSILPPPQGPA PIP\SSTAAGIPRRPRIAWARR/WPLS EPGFRRRESQEEPRAVLAQKIEKET QILNCALDDIEWFVARLQKAAEAF KQLNQRKKGKKKGKKAPAEGVLT LRARPP\PEGEFI\DCFQKIKLAINLL AKLQKHIQNPQRR\DVVHFLFGPLD LIVNTCSGPDIARSVSCPLFSRDAVD FLRGHLVPKEMSLWESLGESWMRP RSEWPREPQVPLYVPKFHSGWEPPV DVLQEAPWEVEGLASAPIEEVSPVS RQSIRNSQKH/RPHFRAHPPGGCPY HQSAPHILTRGYQPTPAMAKYVKIL YDFTARNANELSVLKDEVLEVLED GRQWWKLRSRSGQAGYVP\GNILG EARPEDAGAPFEQAGQKYLGTPQP DPQATPKLPGGT/IDELMQHMDEVN DELIRKI\TTSRAQPQRHFRVERSQP VSQPLTYESG\PDEVRA\FLEAKAFS PRIVENLGILTGPQLFSLNKEELKKV CGEEGFRVYSQLTMQK\AFLEKQQS GSELEELMNKFHSMNQRRGEDQLG PAALGWGLRRGSPPTMHGVLFLYV YVFCIK
3463	8960	A	3732	1	324	
3464	8961	A	3733	1	581	MDKLLETYSLQRLSQEEIESLNRTI MSFKTKSVINTIPTKKSPGPDRLTAN FYQMCKEELADIIIGHLCIRHEMTPV NPGVGQCCTSSYANRRPCFSSLVVD ETYVPPAFSDDKFIFHKDLCQAQGV ALQTMKQEFLINLVKQKPQITEEQL EAVIADFSGLLEKCCQGQ\NQEVCF AEEGQKLISKTRAALGV
3465	8962	A	3734	39	1935	LATMKWVESIFLIFLLNFTESRTLHR NEYGIASILDSYQCTAEISLADLATIF FAQFVQEATYKEVSKMVKDALTAI EKPTGDEQSSGCLENQLPAFLEELC HEKEILEKYGHSDCCSQSEEGRHNC FLAHKKPTPASIPLFQVPEPVTSCEA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YEEDRETFMNKFIYEIARRHPFLYA PTILLWAARYDKIIPSCCKAENAVE CFQTKAATVTKELRESSLLNQHAC AVMKNFGTRTFQAITVTKLSQKFTK VNFTEIQKLVLDVAHVHEHCCRGD VLDCLQDGEKIMSYICSQQDTLSNK ITECCKLTTLERGQCIIHAENDEKPE GLSPNLNRFLGDRDFNQFSSGEKNI FLASFVHEYSRRHPQLAVSVILRVA KGYQELLEKCFQTENPLECQDKGE EELQKYIRE\GQPWAKGSSGFSKK* GEYYLQTGSSLSLQQ*RPPQLTSSEL MAITRKMAATAATCCQLSEDKLLA\ CGEGAADIII\GHLCIRHEMTPGKPL VFGQVPAPPSICPNRRPHASSTWVV DGNIWSPPCISLMTKFHFSP*RDPGG PSLQGW*ALAKPMKAKRFPSLTLV KAKGPQIPGGNNSEAVIARFPQAWL EK\CCQ/GPQEQEVCFAQEGTK\LISK TRAALGV
3466	8963	A	3735	95	272	RALQPDTTWE*GSQRRPWLPQVTN KPVL*SKTSKS
3467	8964	B	3736	344	1420	MLLKTVLLLGHVAQVLMLDNGLL QTPPMGWLAWERFRCNINCDEDPK NCISEQLFMEMADRMAQDGWRDM GYTYLNIDDCWIGGRDASGRLMPD PKRFPHGIPFLADYVHSLGLKLGIY ADMGNFTCMGYPGTTLDKVVQDA QTFAEWKVDMLKLDGCFSTPEEAA QGYPKMAAGLNATGRPIAFSCSWP AYEGGLPPRVNYSLQADICNLWRN YDDIQDSWRSVLSILNWFVEHQDIL QPVAGPGHWNDPDMLLIGNFGLSL EQSRAQMALWTVLAAPLLMSTDLR TISAQNMDILQNPLMIKINQDPLGIQ GRRIHKGSWMPKGSCVPGCLRDPG TQDSQGKISHRSVHAASVQQG*
3468	8965	B	3737	49	2119	MALWTVLAAPLLMSTDLRTISAQN MDILQNPLMIKINQDPLGIQGRRIHK EKSLIEVYMRPLSNKASALVFFSCR TELCLIATTSCLGQLNFTGSVIYEAQ DVLLS*
3469	8966	A	3738	139	536	QSLGFIPPFRKRQRISISYTFYFETGS YSVAQAGVQWHNLGSLQPRPPGFK QSSCLSPPGSWDHWRAPPHQAN\FA LLVETGSPHAAQASLKLLSSSDPSA LASQSTGITGVSHHGQPYISHTLJIIFI GKFY
3470	8967	A	3739	1	213	QFSCLSLPSSRDYRHEQP/PLIFVFLV ETGFYHVGQAGLELLTSGDPPALAS QSAEITGVSPRTRPNNLKS
3471	8968	B	3740	75	729	MEGTAGGERPSVVNGDSGKSGGVG DPREPLSCLQEGSGCHPTTESFEKSV REDASPLPHVCCCKQDALILQRGLH HEDGSQHIGLLHPGDRGPDHEYLLV EEAERAMSEREARPNEESVQRNRLI CRTNPYRIFEYLPLSLEEAFFLVYAL GCLSIYYEKEPLTIVKLWKAFTVVQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PTFRTTYMAYHYFRSKGWVPKVGL KYGTDLLLYRKGPPFYHAX*
3472	8969	A	3741	1	2649	
3473	8970	A	3742	41	656	PVPRPCCGLRARSWPSSPRAARAAL PHGESALSRLLRALLAARASLDLCL FAFSSPQLGRAVQLLHQRGVRVRV VTDCDYMALNGSQIGLLRKAGIQV RHDQDPGYMHHKFAI\VDRRVLITG SLNWTTQAIQNNRENVLITEDDEYV RLFLEEFERIWEQFNPTKYTFFPPKK SHGSCAPPVSRAGGRLLSWHRTCG TSSESQT
3474	8971	A	3743	3	267	FNMESQSLASLKCSGAVSAHCNLCF LGSSNSPASASRVSGITGVLYHTWLI FVFLVQTGFHHVGQAGLELL/NLVI HPPRPPKVLGLQA
3475	8972	A	3744	2	430	FFFETGGAFVTQAGVQWPNLSSLQP SPPGFKPSSHLSLPSTWDYRYTPPCP ASFCIF\TDTGFCHVDQAGLELLASC NLPASASRSAGITGVSHHACPFLLFS FFKSGITSPNYPISHHEIIESNVAPVF LFEDSTAIYVYYF
3476	8973	A	3745	2	316	EFLFFETEFCSVT\RLECSGAISAHCK LCLLGSRHSPASASRVARTTGTRHH AQRIF\VFSVETGFHRVS\RDGLDLL/ NLVIHPPQPPKVLGIRGREPPCPACF FAF
3477	8974	A	3746	1	1053	
3478	8975	A	3747	1	3011	SLQRLPGLMHNLQTFLLDGNFLQSL PAELENMKQLSYLGLSFNEFTDIPE VLEKLTAVDKLCMSGNCVETLRLQ ALRKMPHIKHVDLRLNVIRKLIADE VDFLQHVTQLDLRDNKLGDLDAMI FNNIEVLHCERNQLVTLDICGYFLK ALYASSNELVQLDVYPVPNYLSYM DVSRNRL\ENVPEW\VCESRKLGSF GILGHN\QIC\ELPARLFCN\SSLRKLL GQGHN\QLARLPERLERTSVEVLDV QHNQLLELPPNLLMKADSLRFLNAS ANKLESLPPATLSEETNSILQELYLT NNSLTDKCVPLLTGHPHLKILHMA YNRLQSFPASKMAKLEELEEIDLSG NKLKAIPTTIMNCRRMHTVIAHSNC HRGPFPEVM\QLP\EIKCVD\LSCNE\ LSEVTLP\ENLPSPNCRSLDLTGNPR PCPLITKPLELLNNIRCFKID\QPSTG DG\SGAPAVW\SHG\YTEA\SGVKNK LCV\VALSVNNFCDNREALYGVFD GDRNVEVPYLLQCTMSDILAEELQ KKTKNEEEYMVNTFIVMQRKLGTA GQKLGGAAVLCHIKHDPVDPGGSF TLTSANVGKCQTVLCRNGKPLPLSR SYIMSCEEELKRIKQHKAIITEDGKV NGVTESTRILGYTFLHPSVVPRPHV QSVLLTPQDEFFILGSKGLWDSLSV EEAVEAVRNVPDALAAAKKLCTLA QSYGCHDSISAVVVQLSVTEDSFCC CELSAGGAVPPPSPGIFPPSVNMVIK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DRPSDGLGVPSSSSGMAS\EISSELST SEMSSEVGSTASDEPPPG\ALSENSP\ AYPSEQRCMLHPIWLSNSFQRQLSS ATFSSAFSDNGLDSDDEEPIEGVFTN GRRVEVEVDIHCSRATEKEKQQHL LQVPSEASDEGIVISANEDEPGLPRK ADFSAVGTIGRRRANGSVAPQERSH NVIEVATDAPLRKPGGYFAAPAQPD PDDQFIIPPELEEEVKEIMKHHQEQQ QQQQPPPPPQLQPQLPRHYQLDQLP DYYDTPL
3479	8976	A	3748	1	246	LPTLECSGMISAHCNLRLPGSSDSP\ ASASQVAGITSAHHYAWLVFVFSV EMGFHHVGQGWSRSLDLVIRPPQPP KMLGLQA
3480	8977	A	3749	153	527	LLVFYLPTPSLKGGLRQLDMSLLCQ LYSLYESIQEYKGACQAASSPNWTY ALENGFFDEEEEYFPEQNSLHDRRD RGPPRDLSLP\APPSPAATGFWSPSR GSWEGCDCWEALPTGHAVIICCFS
3481	8978	A	3750	2	377	IPAASTFFCFLRQSLTLWPHAGVQW CGLSSLHPPPPGFMLFSCLSLPSSWD YRRPPPRPAKFSVFLVETGFHRVSQ DGLDLMTS\DPPALASQSAGITGVS HCTRPKEAYFYFLALDPRCKDGVR
3482	8979	A	3751	2	294	LFLHADRLEYSGMTISHLQPQTPGA QGDPLTSSLPREVGLQ/CVCHHTQL FFF/CIFVETESHHLA\RAGLKLLGSS DPTASPSQSDGITGMSHHSCPSTF
3483	8980	A	3752	80	267	RQGLTILPRLVLNSC/RLKLSSHLSLP KYWDYRQEPPCLAISIIFFKKSLIYY LNLAILYFKCK
3484	8981	A	3753	1	972	
3485	8982	A	3754	1	283	PKPQEIELPEAKNR\PWIFNKILGTTV KLMELKPNTCYCLSVRAANTAGVG KWCKPYKVSPGKRGALGVERSPKP REPGLWRLGTPLCPHDSSG
3486	8983	B	3755	346	472	XRNMNILQYCPSSDMWTLFETCDV HIRKQQMVSVEETIYIVGG*
3487	8984	A	3756	1	1346	MSAEEMVQIRLEDRCYPVSKRKLIE QSDYFRALYRSGMREALSQEAGGP EVQQLRGLSAPGLRLVLDFINAGGA REGWLLGPRGEKGGGVDEDEEMD EVSLLSELVEAASFLQVTSLLQLLLS QVRLNNCLEMYRLAQVYGLPDLQE ACLRFMVVHFHEVLCKPQFHLLGS PPQAPGDVSLKQRLREARMTGTPV LVALGDFLGGPLAPHPYQGEPPSML RYEEMTERWFPLANNLPPDLVNVR GYGSAILDNYLFIVGGYRITSQEISA AHFLQGP/RTNEWLQVASMNQKRS NFKLVAVNSKLYAIGGQAVSNVEC YNPEQDAWNF\VAPLPNPLAEFSAC ECKGKIYVIGGYSTRDRNMNILQYC PSSDMWTLFETCDVHIRKQQMVSV EETIYIVGGCLHE\RGPNRRSSQSED MLTVQSYNTVTRQWLYLKENTSKS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GLNFDLCAP
3488	8985	A	3757	3	358	TNSMPPMMSMSYRICAMLKGE/DV QALRRAHQRNVKHMRQLLMDRGL PCHPLPPANINPIRVR/DPHPCPIALS HPIYSWSLTLPNKPTSVAVFNYLLS CLTIPFIASFVSLFEKLSAILD
3489	8986	A	3758	1	164	GSTTPAMEFASLFKKILLIDCRD/RG LALLPRLVLSSWPQVIFLPWPPKFL GLRT
3490	8987	A	3759	3	280	FFFETESHSVA\RLEYRGTILAHCILC RQGSSNSPASDPQVAGTTGTRHRA QLTFV\FLVQMGFHHFGQAGLELPN LGIHPTSASPKCWDLPA
3491	8988	A	3760	3	516	AQHQPMNIFPYPVGVHAPLMNIQR NPFNIHPQLPLHLHTGVPLMQVATP TSVSQGLPPPPPPPPPSQQVNYIASQ PRWKRNCTKLQ\IQEKAAQEVK\LAI KPFYQNKDITKEEYKEIVRKAVDKV CHSKSGEVNSTKVGNL\VKAYVDQ YEYSRKGSQRKLWEGPVSTGKN
3492	8989	A	3761	173	411	
3493	8990	A	3762	438	789	LTWSTPVLPAPTAAP\GKYGNGFQG PSSGNTSSSSHSQRPLMAAVKLAES KVSVAVEASADSSKTDKKLQIQEK AAQEVKLAIKPFYQNKDITKEEYKE IVRKAVDKCVLLECSIQKM
3494	8991	A	3763	1097	4669	ILLGTSCKGYALAHTQEGEEKKQTS GTSNTRGSRRKPAMTTPTRRSTRNT RAETASQSQRSPISDNSGCDAPGNS NPSLSVPSSAESEKQTRQAPKRKSV RRGRKPPLLKKKLRSSVAAPEKSSS NDSVDEETAESDTSPVLEKEHQPDV DSSNICTVQTHVENQSANCLKSCNE QIEESEKHTANYDTEERVGSSSSESC AQDLPVLVGEEGEVKKLENTGIEA NVLCLESEISENILEKGGDPLEKQDQ ISGLSQSEVKTDVCTVHLPNDFPTC LTSESKVYQPVSCPLSDLSENVESV VNEEKITESSLVEITEHKDFTLKTEE LIESPKLESSEGEIIQTVDRQSVKSPE VQLLGHVETEDVEIIATCDTFGNED FNNIQDSENNLLKNNLLNTKLEKSL EEKNESLTEHPRSTELPKTHIEQIQK HFSEDNNEMIPMECDSFCSDQNESE VEPSVNADLKQMNENSVTHCSENN MPSSDLADEKVETVSQPSESPKDTI DKTKKPRTRRSRFHSPSTTWSPNKD TPQEKKRPQSPSPRRETGKESRKSQ SPSPKNESARGRKKSRSQSPKKDIA RERRQSQSRSPKRDTTRESRRSESLS PRRETSRENKRSQPRVKDSSPGEKS RSQSRERESDRDGQRRERERRTRK WSRSRSHSRSPSRCRTKSKSSSFGRI DRDSYSPRWKGRWANDGWRCPRG NDRYRKNDPEKQNENTRKEKNDIH LDADDPNSADKHRNDCPNWITEKI NSGPDPRTRNPEKLKESHWEENRN ENSGNSWNKNFGSGWVSNRGRGR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNRGRGTYRSSFAYKDQNENRWQ NRKPLSGNSNSSGSESFKFVEQQSY KRKSEQEFSFDTPADRSGWTSASSW AVRKTLPADVQNYYSRRGRNSSGP QSGWMKQEEETSGQDSSLKDQTNQ QVDGSQLPINMMQPQMNVMQQQM NAQHQPMNIFPYPVGVHAPLMNIQ RNPFNIHPQLPLHLHTGVPLMQVAT PTSVSQGLPPPPPPPPPSQQVNYIAS QPDGKQLQGIPSSSHVSNNMSTPVL PAPTAAPGNTGMVQGPSSGNTSSSS HSKASNAACKNWQKGKVSVAVEA SA\YSSKTDKKFAKFQEKAAQVVKI WAI\KPFYQNKDITKEEYKEIVRKA VDKVCHSKSGEVNSTKA\ANLVKA YVDKYKYSRKGSLKKTLEEPRVTE KDLG
3495	8992	A	3764	108	253	
3496	8993	A	3765	2	283	RRLFFFFETESRSV\SRLECSG\ISAHC NLH/LPGSSNSPGSASRVAGITGACH HAQLIF\VFLVETGFHHVGQAGLEL L/NLMICPPQPPKVLGLQA
3497	8994	A	3766	1	290	RSTFFFFFLERVYCSVT\RLECSGT\IS AHCNLRLPGSSGSHASVSQVAGITG AHHHTQPIFVFLVETGFHHIGQAGL ELL/NLMIHPPRPPKVLGLQV
3498	8995	A	3767	234	1449	EPGTHDPHLFLQGLLFWQAGGGEG GDGTGPAGGRQICVPPAALAHVRV PGEFLAQVAAAA*AIHDEQRPGKLH HPPG/ELMQRGVASESYMIVAPPMP SSWSSSGTNGPPSPTNLT*PIVHFIFS APTP/TKKTTTNTAMKTATHIPDVQ SAFCSPHSGTQRGDGLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLEAEAAAGAAAE DSGAARGSLQPAPAQPPGDPAAQA SVSNGEDAGGGAGRELVDLKIIWN KTKHDVKFPLDSTGSELKQKIHSIT GIPPDESPRRGGPAGPYQQSQRLEL YAQATEALLKTGAAYPCFCSPQRLE LLKKEALRNHQTPR
3499	8996	A	3768	1	8157	
3500	8997	A	3769	1126	1355	
3501	8998	A	3770	1	1611	MGSRCLNPPPPAHSDTTGKDSFGNI RGAETGQGASACSVTSARVTCGAG SEPHSHRNPGISAQVGLAPSYGAAR GRRRPLALQQSPQERRHVGWNSTR GLLPASLPGTASSQSASATASAALP LKVTGPLARNPTPPWTAAAALATR GQRPEKGLFPGPAPFSLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLEAEAAAGAAAE DSGAARGSLQPAPAQPPGDPAAQA SVSNGEDAGGGAGRELVDLKIIWN

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						KTKHDVKFPLDSTGSELKQKIHSIT GLPPAMQKVMYKGLVPEDKTLREI KVTSGAKIMVVGSTINDVLAVNTP KDAAQQDAKAEENKKEPLCRQKQ HRKVLDKGKPEDVMPSVKGAQERL PTVPLSGMYNKSGGKVRLTFKLEQ DQLWIGTKNGTEKLPMGSIK\NVV\S DPI\EGHEDYHNDGRFQLAPTEA\SY YWVYWVPTQYVDAIK\DTVLGKW QYF
3502	8999	A	3771	482	631	AGGWGPQAPDTPWVGPAGQAGRL HPLRSTKRS/MSVPATRTTVPLTVM Q*RRVCRWCWGPLGHWEAHGFLV SGDVNHFGGPAALLL
3503	9000	A	3772	1	1579	
3504	9001	A	3773	3	486	DRYMLTRDYLTVKVWDLNMEARP IETYQVHDYLRSKLCSLYENDCIFD KFECAWNGSDSVIMTGAYNNFFRM FDRNTKRDVTL\EASRESSKPRAVL K\PRRVCVGG\KRRRDDISVGQLGTF TKKIL\HTAW\HPAE\NIHLPFAATNN LLHLSRGKVNSDMH
3505	9002	A	3774	72	1317	KLLPAPRQPPRPTNGSPRDPTPAQV* VEAPAGSSQ*TAP/ARRPLRAARTLP AAEAAGLTLRGCFHGDRGRACAAL RRWPWRQLRGWGFEVPAPPLLRTP AELVG/RSPEPRCPGKVSMAEFLTEF LEIPPFNKQYTESQLRAGAGYILEDF NEAQVDVLESQFSQLLHQINSTRDF ESIRLAHDHFLSNLLAQSFILLKPSP VEEKSEPQDFQEADSWGDTKRTPG VGKEDAAEETVKPGPEEGTLEKEE KVPPPRSPQAQEAPVNIDEGLTGCTI QLLPAQDKAIVFEIMEAGEPTGPILG AEALPGGLRTLPQEPGKPQKDEVLR YPDRSLSPEDAESLSVLSVPSPDTAN· QEPTPKSPCGLTEQYLHKDRWPEVS PEDTQSLSLSEESPSKETSLDVSSKQ LSPKALAPFQLGN
3506	9003	A	3775	1	350	FGTRKPGAVGAGEFVSPCESGDNT GEPSALEEQRGPLPLNKTLFLGYAF LLTMATTSDKLASRSKLPDGPTGSS EEEEEFLEI\PPFNKQYQESQLRAGA GYILKEFKEAQVRSFFV
3507	9004	A	3776	3	318	RRGLTLSSRLEYSGIIKTHWNLHLL GSSNPPTSASQVAGTTGTCHHAQLN FF/CLTFLVATRSHDIAQAGLELLDS SHPPASASHSAGTTGVNHHAWPAV ALLWIN
3508	9005	A	3777	4	378	ARNHHDLCFKKAILFFEMESCSVSQ AGVQWRVFGSLQAPPPGFLPFS/CY RCQPPSPANFFLYFLVETGFLF**RQ GFTVLDRMVSIS*PRDPPALASQSA GITGVSPRTRQEGHS*R*EENGIG
3509	9006	A	3778	19	418	VEMGFCQADQAGLELLTSGDPPAS VSQSTGITVLSLSFFFETESRSVAQA GVQWRDLGSLQRPPPGFTPFSCLSL PSSWDYRRPPPPRLANFFVFSVETGF

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						HRVSQDGLDLLT/S/GDPPASASQSA GDTGVSQAPV
3510	9007	A	3779	3	331	CFIFYFILFYFETESRSVAQAGVQWR HLDSLQAPPPGFTPFSCLSLPSSWDY RRP/PPRPANFFVLLVQTGFHRVSQD GLDLLT/S/GDPLASASQSAGITGLSH RARPAQVS
3511	9008	A	3780	659	1092	AYNIFQFANRTNTGENLPKTLVIKYI SSTFRSFFFFFFFFLRQSRSVAQAGVQ WRNLGSLQPPPPGFTPFSCLSLPSSW DYGRPPPRPANF/SVFLVETGFHRVS QDGLDLLT/S/GDPPTSASQSAGITG VSHCARPHSVLIKEITQT
3512	9009	A	3781	8	295	GRVSLRHQAGVQWRSLGSLQAPPP RFTPFSCLSLLRSWDHRRPPPRPANL LYFLVETGFHRVRQDGLDLLT/S/GD PPALASQSAGITGVSHRAHPTY
3513	9010	A	3782	1474	1870	SARGITGVSHCTRPFSFFFFFFFFETE SHSIAQAGVQWRYLGSLQPLPPGFK QFACLSLSSSWDCRHAPPRPANFL\F LVEMGFHHL*LELLISSDPPASAFKS ARITGVSHRAWPIRFFLLKNIFKFLN FC
3514	9011	A	3783	60	560	SDNYEKSHNIQEMTGLQSTLLVNN RVQLNFKWELNFFLSFLKQSSTLVA QAGVQWHDLGSLQPPPPGVKRFSC LSLPSSWDYRHVPPCLANFVFLFFL VETGFLHVGQAGPELLTSGGPPASA SQSAGITSVTH\RPLPEDSAFYQCRL NLWQRSPLECRCSLVLKT
3515	9012	A	3784	3	230	FFFKTESRSVTRLECSGAVLAHCNL QLPGSSNSPASASRVAGITRHVPPH\ RLIFVFLVETGFHHVGQDGLDLLTL
3516	9013	A	3785	3	4117	
3517	9014	A	3786	1	457	FPVRNLDLSTYCIGQKEEQLPSYEL YADINHYGGMIGGHYTACAPLPND RSSQRNDVGWRLFDDSTLTTRDQS QAVTRYAYVLFYRRRNSPVERP\PK AGHSEHHPDLGPAAEAAASQ/ATRP WPGPRGG/APRGQPLNASPPLWIGQ TPPLKQT
3518	9015	A	3787	1	298	NNQESCSVTEAGVQWHDLGSLQPP PSGFKQFS/CAQLLSSQDHRHMPPCP ANFYVFLLIAEMGFYHVSQAGLELL TSSDLPALASQSAGIIGVSHRAWAK
3519	9016	A	3788	3	286	FFFFLFETQSH\SHIRLECSGV\ISDYC NLCLPSSSDSLVLASGV\AGTMGVR HNARLIFVFLVKMRFHHVGPRLGP QIPWTGIWIPSHFGPPQSA
3520	9017	A	3789	1	1422	
3521	9018	A	3790	353	470	IPGVSLYSLFSLL\QNIPQSTEILKKL MTTNEIQSNIYT
3522	9019	A	3791	1328	1615	VSLFHAGVQWCDLSSLQPPPPGFKR FS/RLNLLSSWDYRRPLPHPSTFCKF\ VEMGFHHIGQAGLKLLTSGDPPASA SQSARITGVSHRARNCFYVT
3523	9020	A	3792	2	114	CQPGFVMKGPP\HRVQCQALNKWE

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						TELPSCSR\VCLPEA
3524	9021	A	3794	1940	2062	
3525	9022	A	3795	785	892	
3526	9023	A	3796	1	2745	
3527	9024	A	3797	1	3297	
3528	9025	A	3798	1	2202	
3529	9026	A	3799	1	2868	
3530	9027	A	3800	1	3237	
3531	9028	A	3801	1	2001	
3532	9029	A	3802	1	2982	
3533	9030	A	3803	1169	3269	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPTVSAQNLLK LMSNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSGLPFTITSKRITYLGI QLTRDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGGRINLVKMAILP KVIYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALIAKSSLSQKNKTGGI TLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNYLIFDK PDKNKQWGKDSLFNKWCWENWL AICRKLKLDPFLTPYTKINSRWIKDL HVRPKTIKTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIKL KSFCTAKETTIRVNRQPTEWEKIFA TYSSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYAAKK HMKKCSSSLAIREMQIKTTMRYHLT PVRMVIIKKSGNNRCWRGCGEIGTL LHCWWDCKLVQPLWKSVWQFLRD LELEIPFDPAIPLLGIYPEDYKPCCYK DTCTRMFIAALFTIAKTWNQPKCPT MIDGIKKMWHIYTMEYYAAIKKDE FMSF\AGTWMKLETIILRKLSQGQK TKHRMYSLIGGNLTMRTFGHSAGS HHTPGPIMRCGAGGGIALGEIPNVN DELMGTANQHGTCIPMQQNCTLCT CTLKLKV
3534	9031	A	3804	2821	5793	
3535	9032	A	3805	2	256	KRSLSLPSRLECSGVILAHCKLRLLG SRHSPPSDSGAAGTAGARHHARLFF LYFLVFHRVCLDGLDLL/NLVIHLPR SPKVWGLQA
3536	9033	A	3806	1	2406	
3537	9034	A	3807	139	6503	
3538	9035	A	3808	1	3204	
3539	9036	A	3809	77	277	PHPTPCSCPFPWSASSPLT*TH\QALT EEDEW*QAKNSGQAAQGQTPALPL GNLGQVTAPLCPRFIC
3540	9037	B	3810	21	219	MMPRSSRTKSCRSSCVAWSSCMKE NKELRAEAERLGHELQQAGLKTKE AEQTCRHLTAQVRSLGGTX*
3541	9038	A	3811	1	6359	MTLHATRGAALLSWVNSLHVADP VEAVLQLQDCSIFIKIIDRIHGTEEGQ QILKQPVSERLDFVCSFLQKNRKHP SSPECLVSAQKVLEGSELELAKMT

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						MLLLYHSTMSSKSPRDWEQFEYKI QAELAVILKFVLDHEDGLNLNEDLE NFLQKAPVPSTCSSTFPEELSPPSHQ AKREIRFLELQKVASSSSGNNFLSGS PASPMGDILQTPQFQMRRLKKQLA DERSNRDELELELAENRKLLTEKDA QIAMMQQRIDRLALLNEKQAASPL EPKELEELRDKNESLTMRLHETLKQ CQDLKTEKSQMDRKINQLSEENGD LSFKLREFASHLQQLQDALNELTEE HSKATQEWLEKQAQLEKELSAALQ DKKCLEEKNEILQGKLSQLEEHLSQ LQDNPPQEKGEVLGDVLQLETLKQ EAATLAANNTQLQARVEMLETERG QQEAKLLAERGHFEEEKQQLSSLIT DLQSSISNLSQAKEELEQASQAHGA RLTAQVASLTSELTTLNATIQQQDQ ELAGLKQQAKEKQAQLAQTLQQQE QASQGLRHQVEQLSSSLKQKEQQL KEVAEKQEATRQDHAQQLATAAEE REASLRERDAALKQLEALEKEKAA KLEILQQQLQVANEARDSAQTSVT QAQREKAELSRKVEELQACVETAR QEQHEAQAQVAELELQLRSEQQKA TEKERVAQEKDQLQEQLQALKESL KVTKGSLEEEKRRAADALEEQQRCI SELKAETRSLVEQHKRERKELEEER AGRKGLEARLQQLGEAHQAETEVL RRELAEAMAAQHTAESECEQLVKE VAAWRERYEDSQQEEAQYGAMFQ EQLMTLKEECEKARQELQEAKEKV AGIESHSELQISRQQNELAELHANL ARALQQVQEKEVRAQKLADDLSTL QEKMAATSKEVARLETLVRKAGEQ QETASRELVKEPARAGDRQPEWLE EQQGRQFCSTQAALQAMEREAEQ MGNELERLRAALMESQGQQQEERG QQEREVARLTQERGRAQADLALEK AARAELEMRLQNALNEQRVEFATL QEALAHALTEKEGKDQELAKLRGL EAAQIKELEELRQTVKQLKEQLAK KEKEHASGSGAQSEAAGRTEPTGP KLEALRAEVSKLEQQCQKQQEQAD SLERSLEAERASRAERDSALETLQG QLEEKAQELGHSQSALASAQRELA AFRTKVQDHSKAEDEWKAQVARG RQEAERKNSLISSLEEEVSILNRQVL EKEGESKELKRLVMAESEKSQKLEE RLRLL\QAETASNSARAAERSSALR EEVQSLREEAEKQRVASENLRQELT SQAERAEELGQELKAWQEKFFQKE QALSTLQLEHTSTQALVSELLSA\KH LCQQLQAEQAAAEKRHREELEHSK QAAGGLRAELLRAQRELGELIPLRQ KVAEQERTAQQLRAEKASYAEQLS MLKKAHGLLAEENRWLGERANLG RQFLEVELDQAREKYVQELAAVRA DADTRLAEVQREAQSTARELEVMT

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						AKYEGAKVKVLEERQRFQEERQKL TAQVEQLEVFQREQTKQVEELSKK LADSDQASKVQQQKLKAVQAQGG ESQQEAQRLQAQLNELQAQLSQKE QAAEHYKLQMEKAKTHYDAKKQQ NQELQEQLRSLEQLQKENKELRAE AERLGHELQQAGLKTKE\AEQ\TCR HLYLPRLRSLE\AQ\VAHARPSSFRD LGKFQVAT\DALKSREPQAKPQLDL SIDSLDLSCEEGTPLSITSKLPRTQPD GTSVPGEPASPISQRLPPKVESLESL YFTPIPARSQAPLESSLDSLGDVFQD SGRKTRSARRRTTQIINITMTKKLD VEEPDSANSSFYSTRSAPASQASLR ATSSTQSLARLGSPDYGNSALLSLP GYRPTTRSSARRSQAGVSSGAPPGR NSFYMGTCQDEPEQLDDWNRIAEL QQRNRVCPPHLKTCYPLESRPSLSL GTITDEEMKTGDPQETLRRASMQPI QIAEGTGITTRQQRKRVSLEPHQGP GTPESKKATSCFPRPMTPRDRHEGR KQSTTEAQKKAAPASTKQADRRQS MAFSILNTPKKLGNSLLRRGASKKA LSKASPNTRSGTRRSPRIATTTASAA TAAAIGATPRAKGKAKH
3542	9039	A	3812	241	6884	LSGITKMTLHATRGAALLSWVNSL HVADPVEAVLQLQDCSIFIKIIDRIH GTEEGQQILKQPVSERLDFVCSFLQ KNRKHPSSPECLVSAQKVLEGSELE LAKMTMLLLYHSTMSSKSPRDWEQ FEYKIQAELAVILKFVLDHEDGLNL NEDLENFLQKAPVPSTCSSTFPEELS PPSHQAKREIRFLELQKVASSSSGN NFLSGSPASPMGDILQTPQFQMRRL KKQLADERSNRDELELELAENRKL LTEKDAQIAMMQQRIDRLALLNEK QAASPLEPKELEELRDKNESLTMRL HETLKQCQDLKTEKSQMDRKINQL SEENGDLSFKLREFASHLQQLQDAL NELTEEHSKATQEWLEKQAQLEKE LSAALQDKKCLEEKNEILQGKLSQL EEHLSQLQDNPPQEKGEVLGDVLQ LETLKQEAATLAANNTQLQARVEM LETERGQQEAKLLAERGHFEEEKQ QLSSLITDLQSSISNLSQAKEELEQA SQAHGARLTAQVASLTSELTTLNAT IQQQDQELAGLKQQAKEKQAQLAQ TLQQQEQASQGLRHQVEQLSSSLK QKEQQLKEVAEKQEATRQDHAQQ LATAAEEREASLRERDAALKQLEA LEKEKAAKLEILQQQLQVANEARD SAQTSVTQAQREKAELSRKVEELQ ACVETARQEQHEAQAQVAELELQL RSEQQKATEKERVAQEKDQLQEQL QALKESLKVTKGSLEEEKRRAADA LEEQQRCISELKAETRSLVEQHKRE RKELEEERAGRKGLEARLLQLGEA HQAETEVLRRELAEAMAAQHTAES

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						ECEQLVKEVAAWRDGYEDSQQEE AQYGAMFQEQLMTLKEECEKARQ ELQEAKEKVAGIESHSELQISRQQN KLAELHANLARALQQVQEKEVRAQ KLADDLSTLQEKMAATSKEVARLE TLVRKAGEQQETASRELVKEPARA GDRQPEWLEEQQGRQFCSTQAALQ AMEREAEQMGNELERLRAALMES QGQQQEERGQQEREVARLTQERGR AQADLALEKAARAELEMRLQNAL NEQRVEFATLQEALAHALTEKEGK DQELAKLRGLEAAQIKELEELRQTV KQLKEQLAKKEKEHASGSGAQSEA AGRTEPTGPKLEALRAEVSKLEQQC QKQQEQADSLERSLEAERASRAER DSALETLQGQLEEKAQELGHSQSAL ASAQRELAAFRTKVQDHSKAEDEW KAQVARGRQEAERKNSLISSLEEEV SILNRQVLEKEGESKELKRLVMAES EKSQKLEE/RLRLLQAETASNSARA AERSSALREEVQSLRE\EAEKQRVA SENLRQELTSQAERAEELGQELKA WQEKFFQKEQALSTLQLEHTSTQA LVSELLPAKHLCQQLQAEQAAAEK RHREELEQSKQAAGGLRAELLRAQ RELGELIPLRQKVAEQERTAQQLRA EKASYAEQLSMLKKAHGLLAEENR GLGERANLGRQFLEVELDQAREKY VQELAAVRADAETRLAEVQREAQS TARELEVMTAKYEGAKVKVLEERQ RFQEERQKLTAQVEELSKKLADSD QASKVQQQKLKAVQAQGGESQQE AQRFQAQLNELQAQLSQKEQAAEH YKLQMEKAKTHYDAKKQQNQELQ EQLRSLEQLQKENKELRAEAAERLG HELQQAGLKTKEAEQTCRHLTAQV RSLEAQVAHADQQLRDLGKFQVAT DALKSREPQAK\PQLDLSIDSLDLSC EEG\TPL\SITSKLPRTQPDGTSVPGE PASPISQRLPPKVESLESLYFTPIPAR SQAP\LESSLDSLGDVFL\DSGRKTR SARRRTTQIINI\TMTKK\LDV\EEPD/ SAPNLSFYS\TRSAPASQASLRATSS TQSLARLGSPDYGNSALLSLPGYRP TTRSSARRSQAGVSSGAPPGRNSFY MGTCQDEPEQLDDWNRIAELQQRN RVCPPHLKTCYPLESRPSLSLGTITD EEMKTGDPQETLRRA\SMQPIQIAE GT\GITTRQQRKRVSLEPHQGPGTPE SKKATS\CFPRPMTPRDRHEGRKQ\S TTEAQK\KAAPASTKQA\DRRQSM\ AFSI\LNTPKKLGNS\LLRTG*PQRKA LSK\ASPNTRSG\TRRSPR\IATTTASA ATA\AAIGCHPSRPRGKGKALKGPV PVSGPHLCSPMVAVTWSSAYCPSQ CLLSAPRPTVAKPLETVMPARTLA WSLVLHWRLLGAGPGGLEHGQCG RSPYLASFFLKAKSLLHHNQI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3543	9040	A	3813	1	3466	EKEKAAKLEILQQQLQVANEARDS AQTSVTQAQREKAELSRKVEELQA CVETARQEQHEAQAQVAELELQLR SEQQKATEKERVAQEKDQLQEQLQ ALKESLKVTKGSLEEEKRRAADAL EEQQRCISELKAETRSLVEQHKRER KELEEERAGRKGLEARLQQLGEAH QAETEVLRRELAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQQEEAQ YGAMFQEQLMTLKEECEKARQELQ EAKEKVAGIESHSELQISRQQNELA ELHANLARALQQVQEKEVRAQKLA DDLSTLQEKMAATSKEVARLETLV RKAGEQQETASRELVKEPARAGDR QPEWLEEQQGRQFCSTQAALQAME REAEQMGNELERLRAALMESQGQQ QEERGQQEREVARLTQERGRAQAD LALEKAARAELEMRLQNALNEQRV EFATLQEALAHALTEKEGKDQELA KLRGLEAAQIKELEELRQTVKQLKE QLAKKEKEHASGSGAQSEAAGRTE PTGPKLEALRAEVSKLEQQCQKQQ EQADSLERSLEAERASRAERDSALE TLQGQLEEKAQELGHSQSALASAQ RELAAFRTKVQDHSTAEDEWKAQV ARRRQEAERKNSLITILEEEVSILNR QVLEKEGESKELKRLVMAESEKSQ KLEERLRLLQAETASNSARAAERSS ALREEVQSLREEAEKQRVASENLR QELTSQAERAEELGQELKAWQEKF FQKEQALSTLQLEHTSTQALVSELL PAKHLCQQLQAEQAAAEKRHREEL EQSKQAAGGLRAELLRAQRELGELI PLRQKVA\EQERTAQQLRAEKASYA EQLSMLKKAHGLLAEENRGLGERA NLGRQFLEVELDQAREKYVQELAA VRADAETRLAEVQREAQSTARELE VMTAKYEGAKVKVLEERQRFQEER QKLTAQVEQLEVFQREQTKQVEEL SKKLADSDQASKVQQQKLKAVQA QGGESQQEAQRLQAQLNELQAQLS QKEQAAEHYKLQMEKAKTHYDAK KQQNQELQEQLRTLEQLQKENKEL RAEAERLGHELQQAGLKTKEAEQT CRHLTAQVRTLEAQVAHADQQLRD LGKFQVATDALKSREPQAKPQLDL SIDSLDLSCEEGTPLSITRSGGSLPPY VCLWSACCLSGCILVR
3544	9041	A	3814	35	266	
3545	9042	C	3815	383	628	MDPSAGVTIVTCLASLFSGRLVRFR CSHDWRNYTERVLLFQWVELKTKC WRHTEAGLKPSHYFLEKMKKTLRE SQATYDRI*
3546	9043	A	3816	2	513	DIYGGDYERFGLQGSAVASSFGNM MSKEKRDSISKEDLARATLVTITNNI GSTA\WLCALNENIDRVVFVGNFLR INMVSMKLLAYAMDFWSKGQLKA LFF/VEHQGY\LGAVGALLGTVQND

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LMTSRRRGSGRETASQKGQRTKKL LLEKVKVALGRKPSHLWQMNLLGF C
3547	9044	A	3817	29	175	KSRPGTVAHACNPSTLGSRGGRIIPA QEFKTSLGNTVSE\PCLYLRKNN
3548	9045	A	3818	171	419	KFFPFQSLWWERRAFPLKGEDMAA LLCQDEKKDQVERSSTAFHGEIFGT SVPENG\HHPKKQSDGMEEYKTFGL GLTNVKKNR
3549	9046	A	3819	2	1209	WPSKETAFLNTTQMPCLQSASTWS SYEHNSESYLLREHVSELDSSFHSV LSLPSDVPLHFHFETLLKKTEIKGNL AENKFVDEYIISPSPVHSTLNQWRN GYSPICKPQIRSESSAQLLQGRKKRH LSETALGERTKL\KEFDFHHTESGSH SNFTAVSNVNVLSRIQNSSRNTARR R\LRSESSYDI\DNIV\IPMSL\VAPAK LEKLQYKEILTPSWRMVVLQPLDE YNLGKEEIEDLSDEVFSLRHKKYEE REQARWSLWEQSKWHRRNSRAYS KNVEGQDLLLKEYPNNFSSSQQCA AASPPGLPSENQDLCAYGLPSLNQS QETKSLWWERRAFPLKGEDMAALL CQDEKKDQVERSSTAFHGEIFGTSV PENGHHPKKQSDGMEEYKTFGLGL TNVKKNR
3550	9047	A	3820	7	447	
3551	9048	A	3821	1	373	EQQVLRSTCLGVGAKV/L/VEGMVL QYSTQKGILT/ENHIQEINAQ/TTGLR /KTMLLLDILPSRGPKAFDT/FLDSLQ EFPWVREKLKKAREEAMTDLPAGL EEKGRTGRRMGWGAGEEKGQKCQ TVGMRT
3552	9049	A	3822	1	708	TPVWWNSLWGRFPNSQDSGCSFSP PPQRYVVADGEMEARDKQVLRSLR LELGAEVLVEGLVLQYLYQEGILTE NHIQEINAQTTGLRKTMLLLDILPSR GPKAFDTFLDSLQEFPWVREKLKK AREEAMTRPCLAVDRLTGIP\SHILN SSPSDRQINQLAQRLGPEWEPMVLS LGLSQTDIYRCKANHPHNVQSQVV EAFIRWRQRFGKQATF\RTLDNGL\R AVEVDPSLLLHMLE
3553	9050	A	3823	791	1090	HFLHGPLAQEDKSERERWQ\HLAD\ LADFALA\MKDTLTNINNQSFNNFM LRIGEHTPAGLPRSRLPSHAGAWPP TRRDMRLRTTEAIRVGRFTHSQGKE T
3554	9051	C	3824	172	243	MRPSHGPSEQLCSTLSPPIKPRPT*
3555	9052	A	3825	1	615	
3556	9053	A	3826	1	596	PGWEKRMSRSSVVNTQEALPTAAIP RDAKGRVYYFNHITNASQWERPSG\ NS\SSGGKNGQGEPAVV\RC\SHLLV KHSQSR\RPSSW\RQ\EKITRTKGGGP GSLINGLHPEDSSSGEEDF\ESLASQF SDCK/SSAKARG\DLGAFQQKVRLQ KPFLKTPRFAL\RTGGDERGPCFTD\

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SGIHIILPHLSEGGGEPRPGLGAGQGG
3557	9054	A	3827	1	295	ETVFHSVTQSGMQWHNLASLQRLP LRLKQTSHLSLLSSWDCRHMPPNL A/NF/CVLRRDKISPFCPGWASNPPG LKQCIGILKYPQALTPYELINIWEGI
3558	9055	A	3828	131	771	MGVILEPSGTTVPLVSSV*LLVWDH GPTRIVGLIIRLGPR/YPLVSSSSKSG RTMPNILDDIIASAVENKIPPSKTSKI NVKPELKEEPEESIISAVDENNKLYS DIPHSWICDALQKAFTDKEELLKQQ ASNLHEQKKAGVIFEAEEVITLLTS VLKTSSASRTSLSSRHQFAPGATVL YKGDKMVLNLDRSRVPTECIEKIEA ILKELEKPAP
3559	9056	A	3829	1	655	MPVNAGGKVQESQKPPTLIPEPKDS QANFKSSSEQSLTEMWRPNNNLSK EKTEWHVEKSSGKLQAAMASVIVR PSSSTKTDSMPAMQLASKDRVSERS SAGAHKTDCLKLAEAGETGRIILPN VNSDSVHTKSEKNFQAVSQGSVPSS VMSAVNTMCNTKTDVITSAADTTS VSSWGGSEVISS/CIKYHFGLYIIRM CIFKKCQSASGSKTRMQGYLE
3560	9057	A	3830	1	515	LTLENQIKEEREQDNSESPNGRTSPL VSQNNEQGSTLRDLLTTTAGKLRV GSTDAGIAFAPVYAMGAPSSKSGRT MPNILDDIIASVVENKIPPSKTSKINV KPELKEEPEESIISAVDENNKLYSDIP HSWICEKHILWL\RIIIIAVIGSFSKNV GNKDSLQWFLVCIRK
3561	9058	A	3831	6	226	RKGGFFVDLFVR\VSNQVAVNMYK QLGYSVYRTVIEYYSASNGEPDEDA YGKLPSMAVSPRSRNSYILSTDCSI
3562	9059	A	3832	37	611	SGGGAMTTLRAFTCDDLFRV/FNNI NLDPLTETYGIPFYLQYLAHWPEYF IVAEAPGGELMGYIMGKAEGSVAR EEWHGHVT\ALSVAPEF\RRLGLAA KLMELLEEISERKGGIFLVDLF\VRV SNQVA\VNMYK\QLGYSVYR\TVI\E YYFGPATGEP**GTLIDMRESTFPRD TGERNPIIP\LPHPGGGLEDH
3563	9060	A	3833	1	191	MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF
3564	9061	A	3834	2	1203	LSRRCQLSHSVLPPLRRRVSLPVAM EEEIAALVIDNGSGMCKAGFAGDD APRAVFPSIVGRPRHQGVMVGMGQ KDSYVGDEAQSKRGILTLKYPIEHG IVTNWDDMEKIWHHTFYNELRVAP EEHPVLLTEAPLNPKANREKMTQIM FETFNTPAMYVAIQAVLSLYASGRT TGIVMDSGDGVTHTVPIYEGYALPH AILRLDLAGRDLTDYLMKILTERGY SFTTTAEREIVRDIKEKLCYVALDFE QEMATAASSSSLEKSYELPDGQVITI GNERFRCPEALFQPSFLGMESCGIH ETTFNSIMKCDVDIRKDLYANTVLS GGTTMYPGIADRMQKEITALAPST

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MKIKIIAPPERKYSVWIGGSILASLST FQQMWISKQEYDESGPSI\VHRKCF
3565	9062	A	3835	3	412	SRFPEGLFQPFFPG\MKSCGIHETTF HSH/IIKFDVAIR\KDLYANTLLPGGN HQVSGALLTGMQKEIHAPAAQATL RFKIIAPPGSASTRW/VGSVGSILASL STFQ\QMW\ISKQE\YDESGPLHSSTA KCFLNGLSQIA
3566	9063	A	3837	3	480	SHITVLTLNVNGLNAPVKRHRLAN WIKSQDPPVCFIQETHLTCRDTHRL KIKGWRKIYQANGK/QKKAGVAIL VSDKTDFKPTKI/KRQGHYIMVKGS MQQEEQVLRDPQRDLDSHTMIMGD FNTLLSILDRSTRQKVNKDIQELKSA LHQADLIDIYRTLH
3567	9064	A	3838	1	834	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELTIKKLTQN RSTTWKLNNLLLNDYWKYKQPSEN KHLYANKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITRSEIEAITNSLP T/KKSPGPDGFTAEFYQ\MLEVLAR AIRQEKEIKGIQLVKEEVKLSLFADD MIVYLENPIVSAQNLLKLIGNFSKVS GYKI/NVQKSQAFLYTNNRQTESQI M
3568	9065	B	3839	1	543	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELTIKKLTQN RSTTWKLNNLLLNDYWKYKQPSEN KHLYANKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITRSEIEAITNSLP TKK*
3569	9066	A	3840	1	1470	MEQSWVENDFDELREEGFRRSNFS EVKEESRTQPKEAKNLARRDTHRL KIKGWRKIYEENGKQKKAGVPILVS DKTDFKPTKIKRDKEGHYTMVKGSI QQEELTILNIYAPNTGAPRFIKQVLR DLQRDLDSHTIIMEDFNTPLSTLDRS TRQKVNKDIQELNSALQQVDLIDIC RMLHPKSTEYTFFSAPHHTYSKIDH RVGSKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTENRSTAYNLNNLLL NDYGVHNEMKSEIKMFFETNENKD TTYQNLWDTFKAVEIQTTIREYYKH LYRNKLENLEEMDKFLDTYTLPRV NQEEVESLNRPITGSEIEAIINSLPTK KSPGPDGFTAEFYQRYKEELVPFLL KLFQSIEKEGILPNSFYDASIILIPKPG KDTTKKENFRPISLMNIDAKIMNKIL ANQIQQHIKKLIHHDQVGFIPGMQV WFNIGKSINVIQHINRTKDQK\NHRII SIDAEKAF
3570	9067	A	3841	2807	4148	
3571	9068	A	3842	2	1516	WRKIYQANGK/QKKAGVAILVSDK TDFKPIKIKRDKEGHYIMVKGSIQQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EELTILNIHAPNTEAPRFIKQVLSDL QRDLDSHTIIMGDFNTPLSTLDRSTR RKVNKDTQELNSALHQVDLIDIYRT LHPKSTEYTFLSAPHHTYSKTDHIV GSKALLSKCKRSDIITNCLSDHSAIR LELRIKKLTQNRSTTWKLNNLLLND YWVHNEMKAEIKMFFQTNENKDT TYQNLWDTFKAEEVKSLNRPITGSE IVAIINSLPTKRSPGPDGFTVEFYQR CRKAFDKIQRPFTLKTLNKLAIDGM YLKIIRAIYDKPTANVILNGQKLEVF PLKTGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLRKEKVKLSLFVD DMIVCLENPIISVQKLLKLISNFSKV SGYKINVQKSQAFLYINNRQTESQI MSELPFTIASKRIKYLGIQLTRDVKG LFKENYKPLLNKIKEGTNKWKNVP CSWIGKINIMKMAILPKETPSHMQR HT
3572	9069	A	3843	3	120	FIIDKKQKQLKSPSIDEWIK\KMWYI HKIEYHSAIKGIKF
3573	9070	A	3844	2	244	SRLSFPSSWDYICAPPHLANFCIFLV E\RSVAMLPRLVSSSWAQAILPPWP PKAQGFTGMGHHAQSAAGLYIFSG LGSNAI
3574	9071	A	3845	1	2616	
3575	9072	A	3846	1	773	QTSPMIPSIVVHCVNEIEQRGLTETG LYRISGCDRTVKELKEKFLRVKTVP LLSKVDDIHAICSLLKDFLRNLKEPL LTFRLNRAFMEAAEITDEDNSIAAM YQAVGELPQANRDTLAFLMIHLQR VAQSPHTKMDVANL\AKVFGPTIVA HAVPNPDPVTMLQGHQGVQPKVV E\RLLFLGLWEYWEFSFMDGWEQG GTFDPLHVIENSNAFSTPQTPDIKAV PGGGLCVHFTAGEAEIQKGPPSCGQ NKSTAAFNY
3576	9073	A	3847	1	422	CGRVRACGRVREPSSQIHHNMANL FIRKMVNPLLYLSRHTVKPRALSTF LFG\SIR\SAAPRGCGNPGAAVR\SLL SPGLPA/HHLPACGWGFKKQDCPLR KRCKDCY\LVK\RRGRWYVYCKT\H PRHKQKTRCRTLFPPESRT
3577	9074	A	3848	1959	4060	RFFSFFFFFFETESHSVAQAGVQWCN LGSLQAPPPG\SRHSPASASRVAGTT GAHHHARLIF\VFLVETGFHRISQDG LDLLTS*SARLGIPKCWDYRCEPPH LASI
3578	9075	A	3849	1	1320	
3579	9076	A	3850	1239	1733	ALFFSFFFFFFFETESRSVAQAGVQW RDLGSLQAPP\PGSRRSPASASRVAG TTGARHRIFFVFLVEMGFHRDLDFP TS*SA\QGLQA*ATAPGPFLFFFFFFF LRRSLTLLPRLECNGAILARCNLYL LGSSNSPASASRVAGIAGMHHHAR LIFCILVEMGFHHL
3580	9077	A	3851	131	436	VTHLHQKKGSVFFFFFFFFETESCPV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AQAGVQWRDLRSLQAPPPG\SRHSP ASASRVARTTGAHHYTRLIF\VCLV ETGFHHVSQDGLDLQDQFPWSLFLF CPP
3581	9078	A	3852	56	192	KFLFSPKALNSVRKFFQYFPPPKKR/ CPSQNSQVG/CLKSPP*GEKF
3582	9079	A	3853	1	230	FQLHQH\LLNPKHDYRGWAKWNR NSLYEKMKEGERRK\RRSAIPYLQG QRLDNVVAKKSVPQFFPLRVRDPG VKSSC
3583	9080	A	3854	3	126	SCCGVGNQFKGPGGGGG/RGGG/RR NVSGGGAGGRGWKNERKER
3584	9081	A	3855	1	1021	MPRLEAFVNNQTCPKKECGAASEG DTIGKQSELSFGKAKMARETHWPK KVGKLRSTVVKQLPKTFQAISSTET KDQGPIVPAPVKGEGPIVPAPVKDE GPMVSAPIKDQDPMVPEHPKDESA MATAPIKNQGSMVSEPVKNQGLSG\ PGPVKDQDVVVPEH*KGHDSA\LV APW*RIKGP\VVPRSPVKNQDPILPV LVKDQGPTVLQPPKNQGRIVPEPLK NQVPIVPVPLKDQDPLVPVPAKDQE P/TLPG/PLGSETAAPVPAHSHSPPPA GSSPAPPRAPGSGLRLPCSLAPRDLG TRDRAGTVSGALRTMRHPTGGLCQ KGPCWVPPPPLLQIQHFGPP
3585	9082	A	3856	1	448	SSRKDQGLVVSGPVKDQDVVVPEH QRSRFSCQVVAPVKNQGPVVPESV KNQDPILPVLVKDQGPTVLQPPKNQ GRIVPEPLKNQVPIVPVPLKDQDPL VPVPAKDQGPAVPEP\LKTQGP/KGT LSLPTVSPLPRVMIPTAPHTEYIESSP
3586	9083	A	3857	1	573	DPQFISGSPESPIRLWCVGLGNTKVT FTNPKNPVRAVVIHPRHYTFASGSP DNIKQWKFPDGSFIQNLSGHNAIINT LAVNFDGGLVFGAANGPMHLWDW ETWAPIFKRVHA\AVQPG\SLDSESG IFACAFDQ\SESRLL\TAEADKP\IKV YREDDTATEETHPVSWKPEIIKRKR FLMNVEFFLSLFFSF
3587	9084	A	3858	1	589	EDLRKCTFIFIIGGPGSGKGTQCEKL VEKYGFTHLSTGELLREELASESER SKLIRDIMERGDLVPSGIVLELLKEA MVASLGDTRGFLIDGYPRE\VKQGE EFGRRIGDP\QLVIGKE\CSPDT\MTN RL\LQRSRSSLPVDDTTK\TMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTAIDSIIF
3588	9085	A	3859	1	557	KLLSPKQPLLRAQLKTLVRLLCFSH AFVGLSKITTWYQYGFVQTQGPKA NILVSGNEIRQFARFMTEKLNVSHT GVPLGEEYILVFSRTQNRLILNEAEL LLALAHEFQMKTVTV\PWRTTPLTD VVRLVSNASMLVSMHGAQLVTTLF LPRGATVVELFPYAVNPDHYTPYK TLAMLPGHGTSSM
3589	9086	A	3860	323	656	NEELMPKGRLYPPLANIQEVSINIAI

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						KVTEYLYANKMGFPDTQEPE\DKA KYVK/EKGTWAEWNMDSLLPDV\Y EWPEICNQAPPVNTEIEALPLINTFV CSRGTPFFQTRKR
3590	9087	A	3861	1411	1799	GYLQFSFSFFLFFFFFFFFLRWSLTLS PRLECSSVISTHCNLRLPGSSDSRAS ASQVAGTTGAHHHARLIVCV\LVER VFHHVGQAGLEVLTSGGPPTSASQS ARJTGMSHHTRPVICSFQFSDLPHEY F
3591	9088	A	3862	1	1007	MDGGHLFSNLTGKEEVIHKGAKLH PNGYRMAQGSETLVARGGPCRSVE PSAASPQELRGWWEAQALKRWGL MGGVWVMEVDPSWLGAISAIVSSS ASRLLKSVWHIPCPHFLLLRPQLKE AQRRKKQLEERCRVEESIGNAVLT WNNEILPNWETMWCSRKVRDLWW QGIPPSVRGKVWSLAIGNELNITHEL FDICLARAKERWRSLSTGGSEVENE GLCVAVCAQQGHVGVMGFGSDEP SAVSPCEKGKSLAAWVLIFVDFRVG LQKSFQKRKERESTKLQQLWSWCL MLTYFAAFEVFFEENLPKLFAHFKK NNLTPDIYLID/W*FRLLVGC
3592	9089	A	3863	1	1857	
3593	9090	A	3864	1	840	GIPAADR\EASLELIKLDISRTFPNLCI FQQGGPYHDMLHSILGAYTCYRPD VGYVQGMSFIAAVLILNLDTADAFI AFSNLLNKPCQMAFFRVDHGLMLT YFAAFEVFFEENLPKLFAHFKKNNL TPDIYLIDWIFTLYSKSLPLDLACRI WDVFCRDGEEFLFRTALGILKLFED ILTKMDFIHMAQFLT\RLPEDLPAEE LFGPSIATIQMQSRNKKWAQVLTAL QKDSREMREGKSVPPTLRLQREFAL GTNQSPMPRPLCCFRLTPGQPRRTD AL
3594	9091	A	3865	3	288	FFFEMESLYVT\RLNCSGTITISVHC NLCFPGSSDSPASASQIAGITGTRHH AQLILVFLVEMGFC/HISTKQMEVIH PPWPPKVLGLQVVTHDVL
3595	9092	A	3866	285	489	
3596	9093	A	3867	3	425	GSSDPPASAFQVAGSISVCHHTQLIF VFLVEVEFHHVSQASLQL/RDLSLPS SWDYRRPPPRPANFFVFLVEMGFH HLNKAIIKSFACNEIQPLSAVSVARA GWGVFEYVSVYFLCSNSDYFSSNPS IANWMREWPLRLSLF
3597	9094	A	3868	1	156	APPHPAN\FAFLVEMEFHDVGQGDL QLLASSDLPASASQSAGITGVSHCN WI
3598	9095	A	3869	1	526	LAESGEGLVLSGGSLRLP\CIASRFIF SSYYMSGVRQAPGKGLEWVSFIR\A TSVRGRFTMSRDESKNITYLQMKSL RRGMFRGDLG\DWPGGDGHWGAL RIWEPLWIFRCLWKMGLRLGASDG VTEPGGLGSHIWTRCLNKPGVLVM

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AEECVSGAVSVGLQDRCTAANRAI FSLEL
3599	9096	A	3870	2	353	
3600	9097	A	3871	136	315	FKYVLSFLFLASGDGESLDEDSEFTL ARDFEIGHFF\RERIVPRAVLYFTGE AIEDDDNV
3601	9098	A	3872	132	1552	GDKNIQMADHSFSDGVPSDSVEAA KNASNTEKLTDQVMQNPRVLAALQ ERLDNVPHTPSSYIETLPKAVKRRIN ALKQLQVRCAHIEAKFYEEVHDLE RKYAALYQPLFDKRREFITGDVEPT DAESEWHSENEEEEKLAGDMKSKV VVTEKAAATAEEPDPKGIPEFWFTIF RNVDMLSELVQEYDEPILKHLQDIK VKFSDPGQPMSFVLEFHFEPNDYFT NSVLTKTYKMKSEPDKADPFSFEGP EIVDCDGCTIDWKKGKNVTVKTIK KKQKHKGRGTVRTITKQVPNESFFN FFNPLKGKSVASGDGESLDEDSEFT LASDFEIGHFFRERIVPRAVLYFTGE AIEDDDNFEEGEEGEEEELEGDEEG EDEDDAE\FNPKVLIFVLLIIHTFSRR DPSQPAECKQQYEAEAGAWQTGCR DSRPVGGASVLAAAQSRGQSLLHL TRFQVHDFHFHFSFFLIILINLYSGN
3602	9099	A	3873	171	324	
3603	9100	A	3874	3	383	
3604	9101	A	3875	2	314	FFFFISALKALFAFLQILLFQVNVLRI TAHIVISFINLLSVTPSKAFLLLAFIF CREDYSFTAYATISYLKIGPKANLL NN\EAYVIT\MQVTKSTQNSFRVNG Y
3605	9102	A	3876	3	319	TESRSVPQLGVQWRDLGSLQPPPPG FTRFSCLSLPSSWDYRHTPPRPANFL \FFLVETGFRHVGQTGLELLTSGDPP ASASQSAGILCVLCTSTLGNHREHI YRMV
3606	9103	A	3877	118	1341	
3607	9104	A	3878	1	214	GFTSSLACMQMGEMFMGFTCQT\H LLALGCALFTAYLGVGMANFMAE GTCERRIVGKKKASITKDHQQRRI
3608	9105	A	3879	1	176	MRTFALLTAMLLLVA/HAQAEPLQ ARADEAAAQEQPGADDQEMAHAF TWHESAALPLSA
3609	9106	A	3880	3	125	AASTFLFPNLKNSLRG\SLRTFSSVT NVRKTALTWLNSQDI
3610	9107	A	3881	1169	1512	YTQKNWHLFCFIFLRWSFVLVAQP GVQWCNLSSLQPLPPRFR*FSCLSLL SSWDYRCAPPRPANF/SVFLVETGF HHVGQADLELLTSGDLPTSASQSAG ITGVSHCTWPDILYEI
3611	9108	A	3882	43	347	AGVQ*CDLG*LQLLPLGFK*FSCLSL PSSWDYRRLPPRPANF*FLVETGFH HVGQADLELLTSGDSPASASQSAGI TGMSHRAGPI*KSFLKYSTNKLRTT
3612	9109	A	3883	10900	11295	KPWVNETGKLFQDSYSISSHIHLSGF SFPSFFSETESCSVTQAGVQWHDLS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SLKPLPPGFKQFSCLSLPSSWDYRR VPTRPANF/SVFLLETEFHRVSQDGL DRLT/S/GDPPSSASQSAGITGVSHRA RPHSPHF
3613	9110	A	3884	3	227	RFSCLSLSSSWDYRAP\PPRLANFCI LVETGFHHAGQTGLELLTSGDPPAS ASEIAGITGMSHHTQPGQLLWECC
3614	9111	A	3885	2	296	KWSSALVAYAGVTWHHLGSLRSPP PGFKRFCCLSLPSSWDYRHAPPPPA/ NFFVFLVKTGFLHVGQAGLELPISG DPPALAPKQSAWIRGVSHRAQPQN
3615	9112	A	3886	1	162	LGGLVFPSEVVCK/RKLDGMQLIKV HLDKAQQNNVENKAETFSGVCKK HRDLMA
3616	9113	A	3887	2	474	
3617	9114	A	3888	2	592	STGKFSQEKAMFSSSAKIVKPNGEK PDEFESGISQALLELEMNSDLKAQL RELNITAAKEIEVGGGRKAIIIFVPVP QLKSFQKIQVRLVRELEKKFQWES MSVFIAQ\RRILP\KPTRKSRTKNKQ KRPRSRTLTAVHDAILEDLVFPSEIV GKRIRVKLDGSRLIKVHLDKAQQN NVEHKVETFSGVYKKHRDLMA
3618	9115	A	3889	1	93	GFTMLP/RLVLNSWVQMICLPWPPK MLSLQA
3619	9116	A	3890	1	252	PTLEQYAMRAFADALEVIPMALSE NSGMNPIQTMTEVRAR/QDMKQQH VIETLIGKKQQISLATQMVRMILKID DIRKPGESEE
3620	9117	B	3891	18	1121	MASMGTLAFDEYGRPFLIIKDQDRK SRLMGLEALKSHIMAAKAVANTMR TSLGPNGLDKMMVDKDGDVTVTN DGATILSMMDVDHQIAKLMVELSK SQDDEIGDGTTGVVVLAGALLEEA EQLLDRGIHPIRIADGYEQAARVAIE HLDKISDSVLVDIKDTEPLIQTAKTT LGSKVVNSCHRQMAEIAVNAVLTV ADMERRDVDFELIKVEGKVGGRLE DTKLIKGVIVDKDFSHPQMPKKVED AKIAILTCPFEPPKPKTKHKLDVTSV EDYKALQKYEKEKFEEMIQQIKETG ANLAICQWGFDDEANHLLLQNNLP AVRWVGGPEIELIAIATGGRIVPRFS ELTAEKLGFAGLDKRISFGDT*
3621	9118	A	3892	1	282	LPSSTHTIPGYP\NPLHPRPFPSSRLPP GIIGGEYDQRPTLPYVGDPISSLIPGP GETPSQFPPLRPRFDPV/GPNDRFPF RPSRGRPTDGRLSFM
3622	9119	A	3893	3	166	PRPFPKSRLPPGIIGGEYD\QRPNPILP \GRGGPNDRFPF\RPSRGRPTDGRLS FM
3623	9120	A	3894	101	1926	SPVRGRRRLGRELLGPAAVPVAAS GSRPLGPPAAVMRLRVRLLKRTWP LEVPETEPTLGHLRSHLRQSLLCTW GYSSNTRFTITLNYKDPLTGDEETL ASYGIVSGDLICLILQDDIPAPNIPSS TDSEHSSLQNNEQPSLATSSNQTSM

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QDEQPSDSFQGQAAQSGVWNDDS MLGPSQNFEAESIQDNAHMAEGTG FYPSEPMLCSESVEGQVPHSLETLY QSADCSDANDALIVLIHLLMLESGY IPQGTEAKALSMPEKWKLSGVYKL QYMHPLCEGSSATLTCVPLGNLIVV NATLKINNEIRSVKRLQLLPESFICK EKLGENVANIYKDLQKLSRLFKDQ LVYPLLAFTRQALNLPDVFGLVVLP LELKLRIFRLLDVRSVLSLSAVCRDL FTASNDPLLWRFLYLRDFRDNTVR G\QDTDWKELYRKRHIQRKESPKGR \FVMLLPSSTHTIPFYPNPLHPR\PFP\ SSRL\PPGI\IGGEYDPKTNTFPMLGD PISSLIPWVLGETPQPSFPPTETHALN PSWPPISRDPNPQSCPGAEGGPPN/R TRFPPLRPQPGGRANLMAGLVISCG LDLLIFISWSLPFVFCFLNYRCQRPW GADLRVLFS
3624	9121	A	3895	2	442	LSQLCGDPQRFDDFLRAYVEKYKF TSVVAQDLLDSFLSFFPELKEQSVD CRAGPPLAEPDLSQGSSLTRPVEAL FQL/WTAEPLDQAAASASAIDISKW RTFQTALFLDRLLDGSPLPQEVVMS LSKCYSSLLDSMNAEIRIRWLQIV
3625	9122	A	3896	1	1035	GEFLVIDVIHEVAHSWFGNAVTNAT WEEMWLSEGLATYAQRRITTETYG AAFTCLETAFRLDALHRQMKLLGE DSPVSKLQVKLEPGVNPSHLRNLFT YEKGYCFVYYLSQLCGDPQRFDDF LRAYVGE\YKFTSVVAQDLLDSFLS FFPELKEQSVDCRAGLEFERWLNAT GPPLAEPDLSQGSSLTRPVEALFQL WTAEPLDQAAASASAIDISKWRTFQ TALFL\DRLLDGSPLPQEVVMSLSK CYSSLLDSMNAEIRIRWLQIVVRND YYSLT/FHRVRRFPGRARCHACYTIP LYEDLCTGALKSFALEVFYQTQGRL HPNLRRAIQQILSQGLGFQHRARP
3626	9123	A	3897	2	912	CSRSSRTGGWWPAPCSAASRRPTPG PAAAAAATTD/VVTAGCGFGKDFR KGLLKKGACYGDDACFVARHRSA DVLGVADGVGGWRDYGVDPSQFS GTLMRTCERLVKEGRFVPSNPIGILT TSYCELLQNKVPLLGSSTACIVVLD RTSHRLHTANLGDSGFLVVRGGEV VHRSDEQQHYFNTPFQLSIAPPEAE GVVLSDSPDAADSTSFDVQLGDIILT ATDGLFDNMPDYMILQELKKLKNS NYESIQQTARSIAEQAHELAYDPNY MSPFAQFACDNGLNVRGGKPDDIT VLLSIVAEYTD
3627	9124	A	3898	2	220	YMSKKFSALLQSQERNCLIINWCSS LCLRVRLYLRQVTVIPRICKVSD\SP CAPEADAMFAFNADGVGDAKG
3628	9125	A	3899	1	346	SANATTKTSETNHTSRPRLKNVDRS TAQQLAVTVGNVTVIITDFK\EKTRS SS\TSSSTVTS\SAGS\EQQN\QSSSGV

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						QRAPDKGLPPRSLPTPKGDMS\AVN DEIFPEIATWNCEKL
3629	9126	A	3900	76	368	
3630	9127	A	3901	1	1182	MFAKGRGSAVPSDGQAWEKLASY VYEYLLHVRVQKSAETFLSEIRWEK NITLGEPPGFLHSWWCVFGDLYCA APQRRDTCEHSSEAKAFHDYSAAA APSPVLGNIPPNDGMPGGPIPPGFFQ GPPGSQPSPHAQPPPHNPSSMMGPH SQPFMSPRYAGGPRPP\IRMGNQPPG GVPG\TQPLLP\NSMDPTRQQGHP\N MGGSMQRMNPSPRPLGPMGPRPHR ITGSGMRPPPNSLGPA\MP\GINMGP GAGRPWPNPNSANSIPYSSSSPGTY VGPPGGGGPPGTPIMPSPADSTNSS DNI\YTMI\NPV\PPGGSRSNFQMGPG STGPMDSMGGMEPHHMIG\SLGSG DIDGLPKIFPNNISGISNPPGTPRDDG ELGGNFLHSFQNDNYSPSMTMSV
3631	9128	A	3902	2	470	IPTFGLPGSIQSDNGP\SFISQITQQVS QSLGIQWRLHIPCWPQTSGKVERAN GILKAQLTKLTLEVQKPWDL\LLPH RHWESIRRP/GPKGTLLSFSSIWSLIY GTPFPLT\NRPPSNSQLGGIPSQQSSL MEVIFLWPTRPTRAFPKPHGGGLPIP K
3632	9129	A	3903	69	523	PLGCASSQSISASRNTLCTTASSCCP QVLAHS\KAAEYMTRWKVQQMPH SQDRALQSVFCAPFHS**LVALPTG HR*MTPAQFSECFQATSGGSD*DPF LAPSFL\VPGLPVAPGLLLPLGPVHS RATMEEGQATHEELTVFIGLRPGVR GS
3633	9130	A	3904	101	1469	RTHPTFPHPGTGPTSAPPSGALEGTA GTITSNEWSSPTSPEGSTASGGSQAL DKPIDNDGEGVWSPDIEQSFQEALA IYPPCGRRKIILSDEGKMYGRNELIA RYIKLRTGKTRTRKQVSSHIQVLAR RKAREIQAKLKDQAAKDKALQSM AAMSSAQIISATAFHSSMRLARGPG RPAVSGFWQGALPGQAETSHDVKP FSQQTYAVQPPLPLPGFESPAGPAPS PSAPPAPPWQGR\SVASSKLWMLEF SAFLEQQQDPDTYNKHLFVHIGQSS PSYLRPYLEAVDIRQIYDKFPEKKG GLKDLFERGPSNAFFLVKFWADLN TNIEDEGSSFYGVSSQYESPENMIIT CSTKVCSFGKQVVEKVETEYARYE NGHYSYRIHRSPLCEYMINFIHKLK HLPEKYMMNSVLENFTILQVVTNR DTQETLLCIAYVFEVSASEHGAQHH IYRLVKE
3634	9131	A	3905	1	1290	
3635	9132	A	3906	2	270	ISLADLKEGPHTHLKPPDYSVAVQR SKMMHNSLSRLPPASLSSNLVACVP SKIVTQPQRHNLQPFHPKLGDVTDA DSEED\ENEQVSAV
3636	9133	A	3907	2	288	RWGLALSLR/AGAQWFHHGSLQPQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PPMLKSSSRLSLPSSRNHRHTQPCPA NFFIFVEMGFHHVAQAGLELLSS\LT VWASQSAGITGVSHRTHPLLS
3637	9134	A	3908	3	222	FFFETESRSVT\RLECSGTISAHCKLH LPGSCHSPASASRVAGTTGAHCHTQ RIF\VEMGFHRVSQDGLDLKNL
3638	9135	A	3909	3	175	GTSPKDCEVRDFCPSEGLYST*WGG SILPSLDT/FKKMWVSKKKYEEDGA RSIHRKTF
3639	9136	A	3910	2	533	RAAEFFFETFNVPALFISMRAVLSLY ATGRTTGVVLDSEDGVTHAVPIYE GFAMPHSIMCIDIADRDVSRF\LR\L YLRK\EGYDFHSS\SEFEIVKAIKERA CYLSINP\QKDETLETEKAQYYLPD GSTIEISAPQERLYSTWIGGSILASLD TFKKMWVSKKEYEEDGARSIHRKT F
3640	9137	A	3911	1	1213	EFGALRRTRLGSSFPRRRDSSAMES YDVIANQPVVIDNGSGVIKAGFAGD QIPKYCFPNYVGRPKHVRVMAGAL EGDIFIGPKAEEHRGLLSIRYPMEHG IVKDWNDMERIWQYVYSKD\QLQT F\SEEHPVLLTEAPLNPRKNRERAAE VFFETFNVPALFISMQAVLSLYATG R\TTGVV\LDSGDGVTHAVPIYEGFA MPHSIMRIDIAGRDVSRFLRLYLRK EGYDFHSSSE\FEIVKAIKERACYLF HKTPKRD\ETLETEKASVTTWLDGS TIEIGPFR\FRAP\ELLFGPRI*LEKESE GI\HEVPGVRPFRKSDMGPAGARLF SNIVL/SQGGSTPVQKFSSLPISGFGD RLLC*VKKL\APKDVKIRISAPQERH VYPRGLGGSILASLDT\FKKMWVLQ KGDMR*DGSTIEIGPFRIPGPLSCSSG PEFDWKRKVKASHEVPGVRPFRKS DMGPAGARLFSNIVLFREALPLFKS SPLCPFQVLVTGSFVIVKKLSSKRCE DQDICTSGETCISTWIGGLHPCLPGH HLRRCGCSKKEI
3641	9138	A	3912	2	262	LEKRSHSVT\KLGYSGVIIAHCSLNF LSSSQPPTSASQTAGTTGICHSTQLIF KIFLVEMG/LHYVAQAGLDLLGSSN VEPPKVLLGL
3642	9139	A	3913	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3643	9140	A	3914	1	387	TPEKEPPLWHAEFTKEELVQKLSST TKSADQLNG\LLRETEAT\HAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT

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						MLQLSPEEKGKLAAVAQGLQETSIP KKK
3644	9141	A	3915	360	885	NVFVLLEANQRTSTVTLATVSASGQ MPSTEFGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQPRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSAFQTLF
3645	9142	A	3916	1669	4914	
3646	9143	A	3917	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3647	9144	A	3918	1	387	TPEKEPPLWHAEFTKEELVQKLSST TKSADQLNG\LLRETEAT\HAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK
3648	9145	A	3919	360	885	NVFVLLEANQRTSTVTLATVSASGQ MPSTEFGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQPRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSAFQTLF
3649	9146	A	3920	1669	4914	
3650	9147	A	3921	1	246	FLETEFHSVAQAGVQWCHLGSLQP PPPGFKQLS\CLSLPSSWDYRGTPPY LANFCIFSRDGVSLCWPGWSQTPDL KQSSGNL
3651	9148	A	3922	10	476	DRVLLSVAQAGLQWRDLGSLQPPP P/GFKRFSCLSLPNSWDYRCVPPCLA NFFVFLVETGFHHVGQAGLELLTSG DPPLPQPPKVLGAGITGMSHHTWLI SLIFYQTKWRQTAIASVGIPGSPLCH PLPLIRKGVAGKAVLCPRKDGHTH KTQLRP
3652	9149	A	3923	2	465	ARARADSARAARAEFEDIMKRNRA ISSSPISKAVSGASAGDYSDAIETLLT AIAVIKQSRVAK\DERCRVLISSLKD CLHG\IEGQVPTVWGAQLGALSRKR HPFPGERSP\SRSRETSRRHRDLLHN EDR\HDDYFQERNREHERHRDRER DRHH
3653	9150	A	3924	3	218	LPPPLSNIHSTLSTPFLPPPAPL/SP/YP SRASPPSTYSPLPTPPPLPTSQPSTPT LPLPTPPCSTPSGQALFF
3654	9151	A	3925	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST

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						AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3655	9152	A	3926	1	387	TPEKEPPLWHAEFTKEELVQKLSST TKSADQLNG\LLRETEAT\HAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK
3656	9153	A	3927	360	885	NVFVLLEANQRTSTVTLATVSASGQ MPSTEFGGLDSSIQKLIAIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQPRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSAFQTLF
3657	9154	A	3928	1669	4914	
3658	9155	A	3929	1	1542	
3659	9156	A	3930	3	1771	
3660	9157	A	3931	2	1869	RLVVVEAKMAAQAAAAAQAAAA QAAQAEAADSWYLALLGFAEHFRT SSPPKIRLCVHCLQAVFPFKPPQRIE ARTHLQLGSVLYHHTKNSEQARSH LEKAWLISQQIPQFEDVKFEAASLLS ELYCQENSVDAAKPLLRKAIQISQQ TPYWHCRLLFQLAQLHTLEKDLVS ACDLLGVGAEYARVVGSEYTRALF LLSKGMLLLMERKLQEVHPLLTLC GQIVENWQGNPIQKESLRVFFLVLQ VTHYLDAGQVKSVKPCLKQLQQCI QTISTLHDDEILPSNPADLFHWLPKE HMCVLVYLVTVMHSMQAGYLEKA QKYTDKALMQLEKLKMLDCSPILS SFQVILLEHIIMCRLVTGHKATALQE ISQVCQLCQQSPRLFSNHAAQLHTL LGLYCVSVNCMDNAEAQFTTALRL TNHQELWAFIVTNLASVYIREGNRH QEVV\LYSLLERINPDHSFPVSSHCL RAAAFYVRGLFSFFQGRYNEAKRF LRETLKMSNAEDLNRLTACSLVLL GHIFYVLGNHRESNNMGG\PAMQL ASKIPDMSVQLWSSALLRDLNKAC GNAMDAHEAAQMHQNFSQQLLQD HIEACSLPEHNLITWTDGPPPVQFQ AQNGPNTSLASLL
3661	9158	A	3932	2	614	
3662	9159	A	3933	1	4992	VSSNNVLLNSQADDRVVINKPESAG FRDVGSEEIQDAENSAKTLKEIRTLL MEAENMALKRCNFPAPLARFRDIS DISFIQSKKVVCFKEPSSTGVSNGDL LHRQPFTEESPSSRCIQKDIGTQTNL

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						KCRRGIENWEFISSTTVRSPLQEAES KVSMALEETLRQYQAAKSVMRSEP EGCSGTIGNKIIIPMMTVIKSDSSSD ASDGNGSCSWDSNLPESLESVSDVL LNFFPYVSPKTSITDSREEEGVSESE DGGGSSVDSLAAHVKNLLQCESSL NHAKEILRNAEEEESRVRAHAWNM KFNLAHDCGYSISELNEDDRRKVEE IKAELFGHGRTTDLSKGLQSPRGMG CKPEAVCSHIIESHEKGCFRTLTSE HPQLDRHPCAFRSAGPSEMTRGRQ NPSSCRAKHVNLSASLDQNNSHFK VWNSLQLKSHSPFQNFIPDEFKISKG LRMPFDEKMDPWLSELVEPAFVPP KEVDFHSSSQMPSPEPMKKFTTSITF SSHRHSKCISNSSVVKVGVTEGSQC TGASVGVFNSHFTEEQNPPRDLKQK TSSPSSFKMHSNSQDKEVTILAEGR RQSQKLPVDFERSFQEEKPLERSDF TGSHSEPSTRANCSNFKEIQISDNHT LISMGRPSSTLGVNRSSSRLGVKEK NVTITPDLPSCIFLEQRELFEQSKAP RADDHVRKHHSPSPQHQDYVAPDL PSCIFLEQRELFEQCKAPYVDHQMR ENHSPLPQGQDSIASDLPSPISLEQC QSKAPGVDDQMNKHHFPLPQGQD CVVEKNNQHKPKSHISNINVEAKFN TVVSQSAPNHCTLAASASTPPSNRK ALSCVHITLCPKTSSKLDSGTLDERF HSLDAASKARMNSEFNFDLHTVSS RSLEPTSK\LLTSKPVAQDQESLGFL GPKSSLDFQVVQPSLPDSNTITQDL KTIPSQNSQIVTSRQIQVNISDFEGHS NPEGTPVFADRLPEKMKTPLSAFSE KLSSDAVTQITTESPEKTLFSSEIFIN AEDRGHEIIEPGNQKLRKAPVKFAS SSSVQQVTFSRGTDGQPLLLPYKPS GSTKMYYVPQLRQIPPSPDSKSDTT VESSHSGSNDAIAPDFPAQVLGTRD DDLSATVNIKHKEGIYSKRVVTKAS LPVGEKPLQNENADASVQVLITGDE NLSDKKQQEIHSTRAVTEAAQAKE KESLQKDTADSSAAAAAEHSAQVG DPEMKNLPDTKAITQKEEIHRKKTV PEEAWPNNKESLQINIEESECHSEFE NTTRSVFRSAKFYIHHPVHLPSDQDI CHESLGKSVFMRHSWKDFFQHHPD KHREHMCLPLPYQNMDKTKTDYT RIKSLSINVNLGNKEVMDTTKSQVR DYPKHNGQISDPQRDQKVTPEQTT QHTVSLNELWNKYRERQRQQRQPE LGDRKELSLVDRLDRLAKILQNPIT HSLQVSESTHDDSRGERSVKEWSG RQQQRNKLQKKKRFKSLEKSHKNT GELKKSKVLSHHRAGRSNQIKIEQI KFDKYILSKQPGFNYISNTSSDCRPS EESELLTDTTTNILSGTTSTVESDILT QTDREVALHERSSSVSTIDTARLIQA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FGHERVCLSPRRIKLY\SSITNQQR\R YLEKRSKH\SKESAGLTGHPLVTSE HTRRRHIQPPTSATACRQPLMTFCF YGFAYSGPFI
3663	9160	A	3938	2	354	NRILVITSKAGEVIKHGDLRCVRDE GMPIYKAPLEKGILIIQFLVIFPEKPL ALSGKSFLQLEALLPP\RQKVRITDD MDQVELKEFCPNEQNWRQHREAY EEDEDGPQAGVQFQTA
3664	9161	A	3939	204	374	DHGFLIPLTQGDQKGPPRVHPL*AC YHWNQREKVISSCIGCICMSQIKDP LVKKKKK
3665	9162	A	3940	39	385	AGVQWRDLSSPQPPPPGFKRVSCLS LPSSWDYRPQPRLANFC/DFLVEMG FCHVDQ\AGLELLTSGDPPASASQS AGITGVSHRTQPCLLFLKTKTWGK WEKDGMFWEMNGAQDQQE
3666	9163	A	3941	1	200	FETGSYSVT\RLVFSVQISAHCNLCL PGPSDPPTSASEVVGTSVCHR\TQLI VIYPLQLPKLFRLQV
3667	9164	A	3942	2	458	LFYGVYFLFPLNSCILFVSFTVNHLQ IFFFGGGMKSWSVRRLECSGVILAH CNLRLPGSSDSPASASRVAGTTGTC HR\ARLIFVFLVEMG\FHHVG/RRDG LGSPDLVIHPPR\TPKGVGGLQGVSH CGPGPSPQGFYLKIKELGSSQGGEQ FP
3668	9165	A	3943	1	2499	
3669	9166	A	3944	855	2479	PGGSGPGFPTLEGSSKAGRELGIGY EPGSSGVGAPLTPHKKMKKRKELN ALIGLAGDSRRKKPKKGPSSHRLLR TEPPDSDSESSSEEEEEFGVVGNRSR FAKGDYLRCCKICYPLCGFVILAAC VVACVGLVWMQVALKEDLDALKE KFRTMESNQKSSFQEIPKLNEELLSK QKQLEKIESGEMGLNKVWINITEM NKQISLLTSAVNHLKANVKSAADLI SLPTTVEGLQKSVASIGNTLNSVHL AVEALQKTVDEHKKTMELLQSDM NQHFLKETPGSNQIIPSPSATSELDN KTHSENLKQDILYLHNSLEEVNSAL VGYQRQNDLKLEGMNETVSNLTQR VNLIESDVVAMSKVEKKANLSFSM MGDRSATLKRQSLDQVTNRTDTVK IQSIQKEDSSNSQVSKLRE*LQLISAL TNK\PESNRPPETADEEQVESCTSKP SALPKFSQFLGDPVEKGCPKLRTYS P*QGVSKH*KIFQDLFR\KTGQDV\D GKLTYQEIWTSLGSAMPEP\ESLRAF D\SDGDGRYSFLELRVALGI
3670	9167	A	3945	336	519	AALPCEPAFSPLQEVQRGLQDRGQ NQTQRPFFL\NVVQA\VSQEG\ACV\ YAVSELRKEWGRPQ
3671	9168	A	3946	252	2104	LCASSCPFICPPIRPSVCPPAAPLLLG CRAMARGYGATVSLVLLGLGLALA VIVLAVVLSRHQAPCGPQAFAHAA VAADSKVCSDIGRAILQQQGSPVDA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TIAALVCTSVVNPQSMGLGGGVIFT IYNVTTGKVEVINARETVPASHAPS LLDQCAQALPLGTGAQWIGVPGEL RGYAEAHRRHGRLPWAQLFQPTIA LLRGGHVVAPVLSRFLHNSILRPSL QASTLRQLFFNGTEPLRPQDPLPWP ALATTLETVATEGVEVFYTGRLGQ MLVEDIAKEGSQLTLQDLAKFQPEV VDALEVPLGDYTLYSPPPPAGGAIL SFILNVLRGFNFSTESMARPEGRVN VYHHLVETLKFARGQRWRLGDPRS HPKLQNASRDLLGETLAQLIRQQID GRGDHQLSHYSLAEAWGHGTGTSH VSVLGEDGSAVAATSTINTPFGAMV YSPRTGIILNNELLDLCERCPWGSGT TPSPVSGDRVGGAPGRCWPPVPGE RSPSSMVPSILINKAQGSKLVIGGAG GELIISAVAQAIMSKLWLGFDLRAA IAAPILHVNSKGCVEYEPNFSQEVQ RGLQDRGQNQTQRPFFLNVVQ\AVS QEG\ACVYA\VSDL\RKSGEAARS
3672	9169	A	3947	2	97	GLGRWLT/PVIPTLWEAKKGRSPEV RSSRPVKS
3673	9170	A	3948	3	308	PEDSDEKSLSSSVVVHVRRPSRRVP RMPRGSRSRTSRMAPPASRAPQMR AAPRPAPVAQPP\QPCLYEIKQFLEC AQNQGDIKLCEGFNEVLKQCRLAN GLA
3674	9171	C	3949	38	154	MXSNSFWSVPRTRVTSSSVRVSMR CCYDFILCELIRIKS*
3675	9172	A	3950	1	192	GSNAEP/ARPDLTY/QEP/QGTQPAQ QQQPCLYEIKQFLECAQNQGDIKLC VGFNEVLKQCRLANGLA
3676	9173	A	3951	1	254	LMARMQTLKLAVLWASAIGHTWV HAFTGAFSGGSNAEPARP/DITYRSL YEIKQFLECAQNQGDIKLCEGFNEV LKQCRLANGLA
3677	9174	A	3952	1	142	
3678	9175	A	3953	1	325	FFFEMESCSVAHAGVRWA/DLSSLQ SPFPGFKRFSCLGLLSSWDYRRLPP HPANF\YFLVDTGFHHVGQAGLELL T/S/GDPPASASQSAGITGTSHRARPT VNTFNRPPAS
3679	9176	A	3954	3	304	HEGREKRRVLGAEAGGGRSCEIGV PLEWWRPLMRVRVRMCC\LMLML RWGASFAWYCCFLSFCNWL\SSEDT TGLMITFMLRISALLMRSLQNPEAM TLPW
3680	9177	A	3955	3	961	LLLLNSRPRRRDRLVTLESWANDPD YLKRQVGFCAQWSLDNLFLKEGRQ LTYEKVNLSSIRAMLNSNDVSEYLK ISPHGLEARCDASSFESVCC\SFCVD AGVWDYEVTVVTSGVMQIGWATR DSTFLNHEGYGIGDDEYSCAYDGC RQLIWYNARSKPHIHPCWKEGDTV GFLLDLNEKQMIFFLNG/TPA/RPPEE QVFSSTVSGFFAAASFMSYQQCEFN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FGA\SPFKYPPSMKFSTFNDYAFLTA EEKIIL\PRHRRLALLKQVSIRETAGS LCCDEVADTQLKPCGHSDLCMDCA LQLETCPLCRKEIVSRIRQISHIS
3681	9178	A	3956	4	101	RQSLAMLSRLA\LNSWPQVILLPWP PKVLGLQA
3682	9179	A	3957	21	338	HPVLAITLSIFIFVAFAYAEEELDEIQ P/CIMMKTLNKLGIEGMCLNSIKAIY /DKSNANFILNKEKLKAFFLRSGTRQ IRPNFQ/PLLFNIVLEVLAKEIRQEEEI KV
3683	9180	A	3958	90	360	ALICLVDIESGENSTTRPRFASHDQV CIALLRTA\GILCLETFIDSPSHGSRH FLFVLSSPPLTLFPLLHIYLLAVVVPI VSPLLSLSDPP
3684	9181	A	3959	1	424	CGRRFSTRSDLTKHRRTDTG\EKPN\ RCELCGKRFTCVSNLNVHRRNHAG HKPHKCPECSKAFSVASKLALHRKT HLGERPAECARVGQVLQPQPAPLS QHQRGPHAPPAPLPPLPSSPAVGHC PQSFEGGRLEQEKAKGSL
3685	9182	A	3960	153	328	SIASYFTLVCHLLRKCHPRLGTVAH TYNPSTLGGRGRWIMR\QEFETSLT\ NMVKPCRY
3686	9183	A	3961	1	936	
3687	9184	A	3962	1	1023	
3688	9185	A	3963	15	337	RINNTISWLIYVCKFCLSSFSIYLIIIIII IIFFETESHSVAQAGVQWRNLGSLQ PPPPRFKRFSCLSFPSSWDYRCPPPR PANFCIF\SRDGVSPCWPGWFRTPDL R
3689	9186	A	3964	3	1105	HASALTPVVCMLSAIAFSNVFEHYL GDDMKRENPPVEDSSDEDDKRNQG NLYDKAGKVRKHATEQEKTEEGLG PNIKSIVTMLMLMLLMMFAVHCTW VTSNAYSSPSVVLASYNHDGTRNIL DDFREAYFWLRQNTDEHARVMSW WDYGYHIAGMANRTTLVDNNTW\ NNSHIALVGKAMSSNETAAYKIMR TLDVDYVLVIFGGVIGYSGDDINKF LWMVRIAEGEHPKDIRESDYFTPQG EFRVDKAGFPTLLNCLMYKMSYYR FGEMQLDFRTPPGFDRTRNAEIGNK DIKFKHLEEAFTSEHWLVRIYKVKA PDNRETLDHKPRVTNIFPKQKYLSK KTTKRKRGYIKNKLVFKKGKKISK KTV
3690	9187	A	3965	1	181	ANVVFTQLLIWYGVDVRSRDARGL TALAYARRAGSQECADILIQHG\CS AEGCGLSSTCY
3691	9188	A	3966	640	961	DGVSASCCPGLGVQWVRFLGSL\QP SASWGFKQFSCLSLPSSWDYRRALP PPRPANF/SVFLVKMGFLHVG\QAG LELLTSGHPAASASQSAGITGVSHR TRPAASILI
3692	9189	A	3967	2	334	VGLYGRIEASSPMGEGNRW*SGTPA NQG*QEQGIARPKPRGEPGLRNEGG

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						PGAILPGRWAGV*GPTGQEGR*RGS QESCPCPAQSSCSHRVAGLDVGGSH GHSAAFPATP
3693	9190	A	3968	1	361	ARARLRHLRDLRAPAGPVGGLCAA GTACGWPGPGPLLGERVRAFLRR* RAQHLLHHHRVRAPLPGWREAAG GAPPFLGTYGPESQVRLRDAVVPEA GGQDSGSSGSASLRPRSSFSCSCS
3694	9191	C	3969	151	373	MPTAVXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXVLPFLV LEVMQCLCPVLLLYYDPNSKTRYV FFKTR*
3695	9192	A	3970	50	441	IPSPPDGFFSNLGTRKPFFPCNFSCQ NILLLTRKILLKSFLYPFFFLRWSLA LPPAVLSAHCNLCPPGSSDSLASAS* VAGITGVHHQAWPVLPFLVLEVMQ CLCPVLLLYYDPNSTPRYVFFKTRT FIA
3696	9193	A	3971	3	224	FLRWSLALPPAVLSAHCNLCPPGSS DSLASAS*VAGITGVHHQAWPVLPF LVLEVMQCLCPVLLLYYDPNSFV
3697	9194	A	3972	1	214	PIQFKQRLPFGFLFVFVF*EGVLLCH PGWTAVTEDRSWLTATSTSWAQVI LQSSCLSLPGS*DYRQCLPGV
3698	9195	A	3973	154	341	KNFFRGQFWFVA*AGVQWGHFRSL QPQPSGVKQFFPLGLPKPLDCRCES HRVPFLFLGLETL
3699	9196	A	3974	3	379	FALVAQAGVQWCSFDSLQPPPPGF K*FSCLSLPSSWNYRHLPPRLANFV FLVEMGFHYVGQASLELLTSGDPPA SASQSAGIRGLSHCTWPHVSGFIMQ YEYTLCFMVFIMSFWRNCRKVAKY LK
3700	9197	A	3975	2	35	LKQAPCLCLPSS*DYRHLPPCLSNF* NFL*R*GLSLLPRLVSNS*PQAICPRR PPKVLRL*AQTSPLPLPTK
3701	9198	A	3976	1958	2316	IHSSPTKATFFLRQSLALSPRLEYSG AISAHCNLCFPGSSDSRALAS*AAG TTGACHHIRLIFFLFFVFLVETGFHH VGQAGLELLVSSDLPILVSLSARITG VSHHAQPPPKLLNALL
3702	9199	A	3977	2	80	SLCICMCVCACIRTHA*MYVCVCV HTHACMNATSPSWVF
3703	9200	A	3978	123	452	KTGSNFAPQLEAQGGNLG*LNPWP PG*KQFSGLTLLITWINGAPPPPRAN FGIFNKKGVTPCGQGGPKTRDLGIG PSKPPKGLEFRAQPPEPALMGKFYP MVNLSNVPPF
3704	9201	A	3979	3	250	AIAAH*NLHLLGSSNSSASVSRVAGI TGARHHTQLIFVFLVETGFHHVCQA GIEFLTSGDTSTSASQSARITGMSHH TWPKQ
3705	9202	A	3980	2	257	PRSSPTCPACLCVQVNPPAQDPEDP APQLSPQPQDPAKPPPQPYNPYKPY PNLGCGL*PQNYCIIVCMVSIVYYH MGIIETVKSQ
3706	9203	A	3981	2	147	LVEMGFHHVSQAGLKLLDSGNLSA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						S*RSAGITGISHRAHPPNSTNIYA
3707	9204	A	3982	3	446	QVVRGFGRVSKQMGIPTANFPEQV VDNLPADISTGIYYGGASVGSGDVH KMVVSI*WNPYYKNTKKSMETHIM HTFKEDFYGEILNVAIGD*LRPDKN FDCLESLISPVQGDTD*AKIRLELPE HLRI*EDTFFQVSLNRTMIVTDDK
3708	9205	A	3983	1	162	FFFRVKASICCPGWSTVAQ**LTAA SDSWAQKSSCFSLWSSWDNRRGLP HLANK
3709	9206	C	3984	131	442	MNIPLSMSLVVSNSMQDVFWXXXX XXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXX XXXXXKXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXX*
3710	9207	A	3985	141	429	TGSHFVAQAGMQWCNLWSMQLLP AGLR*FPYLSLPSSWDYRHAPPCST HFLYFFVEMGFCHVAQVGLELLAS SDVPTYASQSAGITGVSNHPRPF
3711	9208	A	3986	1577	1879	
3712	9209	A	3987	1	219	EM*SCRVTQAGVQWCNLSSLQLPS PGFKQFSCLSVPSGWGYRCMPPHP ANFCIFSRDRASPRWPGWSQTPDLR
3713	9210	A	3988	1	414	FF*TGSCFVSQAGTQQQDHSSLQP* TPGLKPSSHLCLLSSWDNRHLIFKFF VEMGSRHVAQAGLQLLGSNNPPTL AS*SARIISWSHRAQPTCTLCSWLC DSGAGTAESFLWQPALSRVANRGC CRRPGKLKEKQGT
3714	9211	A	3989	3	666	FFVETGFCHVGQAGLELLGSGNLPA AASQSAGITGMSHRVRQHS*YETHR KVFYS
3715	9212	A	3990	1	436	FFFFFLRQNLTLSPRL*CSGTILAHC NLQHPGSSDSPASASQVAGITGVRH HIWLIFVFLVEMRFHHVGQASLELL NSGYLPTSASQSAEITGVSHCAQLQ PGILMHGLRRLTDLDDNVHHPRSRL KVTSSSAHPGAASSSFLHL
3716	9213	A	3991	167	563	SESASEFSIFYLFIIIIIIIIIIIIETRSCSVA QTGVQWCDHGLLQPRPPWFRPSCH LSLLSSRDYR*APPHPANTFNFFLLE IGSHYVAWGSLELLGSSDPPASASQ SVEIIGVSHRGPDSQKSFIHLSPRFP
3717	9214	A	3992	3	456	
3718	9215	A	3993	78	129	
3719	9216	A	3994	96	251	MDQYSRNSPLEVNGQQLLGWYQH ALRCKWNF*APLCYCSHTVFNSQPT HTEE
3720	9217	C	3995	94	351	MKRISTTQYYHCQDYDLRHSKHMF CLVSTAFQKVKPLYKYLEILQENLD PQGKDSRWFSVISSPRSQNVKVWR HLQSCLTSHCKH*
3721	9218	B	3996	1	431	MAVASTKSRWETGEVQAQSAAKT LSCKDIVAGDMSNKSFWEQKGGSK TSSTITAQIAFLQGERKGQENLKKD LVRMIRMLEYALKQKRAKYHKLK YGTELNQGAMKPPSYDSDEAQQQA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MRSVHGPLHILSAPPASQQKRPTER *
3722	9219	A	3997	772	1391	IANNKDALRKTWNPKFTLRSHFDGI RALAFHPIEPVLITASEDHTLKMWN LQKTAPAKK*EYSTLTLFEYFK*HA
3723	9220	A	3998	3215	3491	SAKVLRPTFFFFFFFFFFFFAIESHCVT QAGVQWCNLASLQPSPTEFK*FSCL GLPSSWDYRCVPPHPANFYIFSRDR VSPCWPGWSKTPDLK
3724	9221	A	3999	1	779	MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEEK VPETTRFWAPGVEAPGDDAERRR REASGPATRHSPLPTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQEESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF
3725	9222	A	4000	1	1286	MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPGPLGLLGV RPGMPPQPQGPAPLRRPDSSDDRYV MTKHATIYPTEEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAII LNSCVEPKMQVTITLTSPIIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCVIIR ILRDLCQRVP\TWS\DFPSWAMELLV EKAISSAS\SPQSPGDAL\RRVF\ECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PDPASRED/LSTSQCHSLPLETS LAFPPRYHKV\LGMDPITRK*AQRF NI\HNNRKRRRD\SDGVDGFEAEGK KDKKDYDNF
3726	9223	A	4001	2	379	DLPASATQNAGITGVSHHIWPRIIFL LW*KTFTILTFLSVQYSSSNYIHPVC NRALELFKSYKTETKLNFPSPPPPIP VNLHCIFFF*GLTFLLGFFSLPKYRG FTNFVSPCTVAMLTRGGGGGEF
3727	9224	A	4002	229	445	RPGPNFGLLETLTWGLKGTLWLNP PKNWELGAHPPTPGNFWIF*KGGF WNVSQGGSKTRGLRELPPFSWKKG
3728	9225	A	4003	192	529	HEVLNFLTSCVLTTLVFLIADIIWLS CRTRSLPFVATTLEVLPLSLIGLCHH TILVFISNAFFI*KAYFVTSSFIMFP*S FFLFNISVLSYMYLTFSHLTSFVIAY FSYSHI
3729	9226	A	4004	330	754	SDLSQKESSSSLSKFLVTEKNSSLGS GGCDMANKENELACAGHLPEKLH HDSRTYLVNSSDSGSSQTESPSSKYS GFFSGGFLRDHETM\AQVLFSRDMR LNVALTFWRKRSISELVAYLLRIED LGVVVDCLPVLTNCLQE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3730	9227	A	4005	296	861	VSQDHETMAQVLFSRNMRLNVALT FWRKRSISELVAYLLRIEDLGVVVD CLPVLTNCLQEEKQYISLGCCVDLL PLVKSLLKSKFEE*CY*WVLTGLQA VIKRWWSELSSKTEIINDGNIQILKQ QLSGLWEQENHLTLVPGYTGNIAK DVDAYLFPVTIEGFHLLKSIWFFKTS LELYNLQKKKVSV
3731	9228	A	4006	2	265	NNFFSFSETESHSVTQAEAQWYDNS SLQP*ILGLKQSFCLSLPSNWDHRC APPHPQFSFLIPGLYVSQFILGNKPSS LPCQMFKSAV
3732	9229	A	4007	3	295	HFNLSHRSAQAKGNRYKEAEALTN AAVHVDDMPNALNALIDLRAHNLG QDPVNFKRLSHCLLVTLAAHLLAEL TPAVHA*LDKFLASVSTVLTSKYT
3733	9230	A	4008	1	1077	
3734	9231	A	4009	3	285	ETESRLATQAGVQCCDLGSLQPLSP GFK*FSCFSLPSSWDYRYPPSCQAN FCILVEMGFHHVGQASLELLTSGDP PASASQSARITGVSHRAQ
3735	9232	A	4010	1	338	VIATYHGGLCTQKSQPPPPQALWSA STSTINLMVSTEPLALTETHICKLPK D*GTCRDFILPWDYDSNTKSCARF WYGRCSANENDFGSQSECEKVCAP VLCKPGVISEMAT
3736	9233	C	4011	269	526	MLARLVSNSLPQVIHHTQPRVGSPT RIPTLSLNLPLPLALTSLRWDRHQLR GQGHWGAQELRAITGFKDHQVWQ TLNCSLCVPKP*
3737	9234	A	4012	2	51	
3738	9235	A	4013	83	5229	
3739	9236	A	4014	3	45	EVVHALRCRWWSWGLKLDLLTPEP EPICGPALLSRSSLRGSHPTAFLLPP QVSQ*RGELGPSTFRAFRAEFPTSRG SKDNKEKNQQEQDMAKPATGTGQ G*GADGGAGA
3740	9237	A	4015	3	323	LLWKVESSWRDQKDIMSWEWDKR RRRHHLTDRSQLCSKVKFQVDCDLI EWGTWIINLKQYNAYHCEGECHNP VG*KFHQSNHAYIQVGCQVLGGEE AVIWHWGTGL
3741	9238	A	4016	2	279	FFFFEAKSHSVTRMLECNGAISAPC NLHLPGSSDSPASASQVVGITGVYH HTQLIFIFSVETGFCHVGQDGLNLPD LMIHPPWPPKVLG*QA
3742	9239	A	4017	166	939	
3743	9240	A	4018	2	225	KELTGRRCAEPPHPRPSPQLLTEEPF TKGRFSGEWRGRNAASMKTGPFAE HSNQLWNISAVPSWSKVNQGLIRM YKAEP*EGADRKALCRASPPPPIPPV TDRGAIYKRPILWGVERQERSVYED WPICRALQPAVEHQRRPFLVQSEPG SHPHV
3744	9241	A	4019	142	1336	KARGDCKHPGRCWPEQMAEGERQ PPPDSSEEAPPATQNFIIPKKEIHTVP DMGKWKRSQAYADYIGFILTLNEG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VKGKKLTFEYRVSEAIEKLLALLNT LDRWIDETPPVDQPSRFGNKAYRT WYAKLDEEAENLVATVVPTHLAA AVPEVAVYLKESVGNSTRIDYGTG HEAAFAAFLCCLCKIGVLRVDDQIA IVFKVFNRYLEVMRKLQKTYRMEP AGSQGVWGLDDFQFLPFIWGSSQLI DHPYLEPRHFVDEKAVNENHKDY MFLECILFITEMKTGPFAEHSNQLW NISAVP\SW\SKVNQGLIRMYKAECL \EKFPVIQH/FSKFGSLLPIHPVHVGL GGAKPKEPPRGTVSCCLPFPTPAVA PPPSPPSVSSRLMRGCLLGLGGEMG LRGLRA
3745	9242	A	4020	80	283	
3746	9243	A	4021	61	626	DLICVIGVPEEEKETGAKNIFKEIMG ENSPHLVKDVIVHIEEIHSQIDEN*** Q*KSYK**QKGIIIKLRVDLLETMEA KCSRTPSLKCLGKESFGESWESRILH PAEISHRNECHMKIILDFKSEKGPDA VAHTCNPSILGGHTAGGSLEARSFE TNLPETLSLLKKLNLKEKEFVASYP PLVEMLK
3747	9244	A	4022	18	161	TSFKNPPPPPPGGLKKIPSPPPPKKK KFKDVS*PTYYFLYLNASSVT
3748	9245	A	4023	30	262	NRRQAGPFPAKLGRPSPKGGFPNFF KSSSSKSSF*KNPKGQGWGFPPLIPG FQGPQVGGSLGAPGLKPPWGTPQN PF
3749	9246	C	4024	193	366	MYNYRSIPKNKYTYTYTKSYPNKIF SRLILYIPLGTVSQISTLNCVPRFVLL TWKAL*
3750	9247	A	4025	3	258	TIDSLLKGLPCKQNEPWHTIQCGYL GNSSKWNI*YQSGKDFIRIAFCVCIC I/CYF*E*IYSCT*IPVRNTLNELNPLA KCPCPFH
3751	9248	C	4026	164	313	MEGTRIFGKWVKLIQSIPNRNSCTTI DLFLKINIHIHTQKAILMKSFPD*
3752	9249	A	4027	9	373	DRVSLCRPTLEVQWRDLGSLQPPSP QVQSNSPALSLPSSWDYRRVPPCPS *FFVFLSRRWRFHRVGQTALFLIKM MGKKILKIKSNYTLGLYVGPSYSER MIKPQEFESSLGQHCKTPSQK
3753	9250	A	4028	1	336	DRILLHRPCWSTLARS*LTIPSNHLG SVFPPSALLES*DCRHTPTTPD*FLKI FL*RRGLTVFPRLVLNAWTQAIIQPL PLKALGLQDTFFKNINCDRLKVSEY YSDTEIEI
3754	9251	A	4029	514	742	LPKC*DHRHEPPHQAKFFNFFVEMG SCHVPQSGLQLLGSSDLPASAFYSA GIAGMSHHTWPPYLFKSRHKSRFCP S
3755	9252	A	4030	1	264	QAQGKHPGSFGPPFAGLKGFPGLGF PRTGNSGGFPQGGKYKGFLIKNGVP PSFQGGF*IPGPGSHQRLGFRG*VGR AL*TPGFRATLF
3756	9253	A	4031	7	417	RQDLALSPRLECSDTIIAHCSIKLLG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SNGAPSAAS*VAGTTGTRHHAQLIF LKIFVETRSLYVAQASCVFPASSNPP TSASQSTGITGMSCCARPTSYVPGS DLSVLCILTHLILKIPLYRRYYYFVS LTYSKAEVQ
3757	9254	A	4032	123	376	KTGSNFVPQAEAQGGNSG*LNPLPP G*KQFSGLTLLITWINRAPPPPRANF GIFKKKGVSPCC*GGLKTPNSGFSPF KPPKGLE
3758	9255	A	4033	3	292	QWHKHGLLQPQPPGLK*SSHLSLPR SWDHRHVSPCLTNFF*FSVSMGSCY VAQAGLKHLASSDPPASASVGTIG MSTT*SKTTLYTEKLANIILTK
3759	9256	A	4034	1	230	FFF*TDSCSVAQAGLQWRDYRPEPP CPANFITIKQVQNKSVTFPARNLNK MRGASIMLYPIGLSLNDLMQLLSEG F
3760	9257	A	4035	3	189	SWDYRRLPHARLIFVFLVGTGFHHV VQAGLELLTS*FTRLGLPRCWDYRR EHIAPGHIWTY
3761	9258	A	4036	2	148	PGSSNPPTSASQLAGTAGTHHHA*LI FVCLVETGFCHVA*AGV*VKFF
3762	9259	A	4037	348	696	AEEQDKKGRQ*ERGKEWERETETK IYSRIKGNREGQAKKKWGHGELIH KTKDEKRKKSEEDKKLRWRKR*TN SQKD*IRKRLHKETANSER*EEKHK ERKQWRRGPKARRAISRG
3763	9260	A	4038	1	295	QNQFFIFIYFKTESGSVTRLEYSGVIS AHCNLCHPGSSQSPASAS*AAGTTG AHHHIQLLFVFLVETGFHHVGQAG LELLTSSDLPASASQSAWGLQV
3764	9261	A	4039	6	151	SQGLALLPRLISNPWVQAILLPWPP KVLGL*AEIAQNKMQK
3765	9262	A	4040	101	318	SNHTLGTS*HFFFETVSCCIMLHRVE CSGAVIAHCNLELLGSSDSPASTS*V AGTTAVYHHTGLSWLLNHLH
3766	9263	A	4041	210	306	SWPGTVAHICNPSALGGQGGWIA* GQAFRQA
3767	9264	A	4042	2	147	DFSVKTL*ARREWRDIFTVMKEKNF YPRKVYALKIPFKNEAETKKVEV
3768	9265	A	4043	160	525	NTQTRSFGNRLMAPAQSSHKALTK KVMTNCPSETVHDSQECFFVLFFET VLVCLPGWSAVMLVRCSLCLLSSW DYRRVPPHLG*FLYF**R*CLTMLA RMVSNS*PQVIHLPRPPKLLGLQA
3769	9266	A	4044	3	72	KTQVHFQGWQHSVHIITHPCWEKL ALSITPLR*DNRKLQAWNSPRLGPT CLFPRLALMCVLML**NIHEYNSFQ RVLWVLLVNC*ISKVGSTLCISSHIP AGRS
3770	9267	A	4045	313	358	
3771	9268	A	4046	7	308	AGGRRARAPHLGGRGAARGRL*RV RGHRERGLRAAPVPRPQPQLRRGA AAGAVQPGQGVGRAGPPEGSEGSV AGVGLDLDSSCYHHSSDFYICHPMP ISS
3772	9269	A	4047	92	390	ETGSHSVNLAGLQWCDHNSLQP*T

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						PGLKQSSYLSLLSS*DYRWVPPCPA NF*IFFVEIRSCHISQAGLDLPRPSDP PVWGSQSAGTIGMSHHAQPREIC
3773	9270	A	4048	65	375	SQLTATSTSRVQ*HDLSSPQPPPPGF KRFSCLSLPSGCDYRHPPPHLANFL YFLVETGFCHVGQAGLELLTSSDLP ALASQSAGITGVRYCAWPTFLIMKT CIPSFPLPSTSPIPLP
3774	9271	A	4049	12	292	DIVSPVA*TRMQWHNLGSLQPPPPR FKQSLCFSLPSSWDYRCVPPCPAIFF VFLAEMGFCHIGQAGLELLASSNPT TLASQSAEPPHLAATDF
3775	9272	A	4050	40	343	SSSSLILSSSVIYLLLNLSIDFLVLLLY FLVFRFSVCSFCFQFFVKNFNLIFYF FKHIKNICFKVCV*RLGFLDPLCAYF GCLLFL*VFSHVLSLHIPDDL
3776	9273	A	4051	97	282	
3777	9274	A	4052	3	336	FFETGSRFVTHAGVKWHNHDSLHP QPPRLK*FSYFSLLLSSWDHRHVPP RPANLVYLL*RGGPPSMLPRASLEF PGLQVNSSLPSALPKVLGITG*GHRP RPKVTFHQRG
3778	9275	A	4053	3	294	CCFGDGVSLCRPGWSIECSGNHSSL QAVEPPRLR*SSRLSLLGSWDPSHV PLHLANF*TFCTHGVLAMLPLAGLK TPWAQTIPPHLSLPKVLGLQG
3779	9276	A	4054	16	308	MPQPN*SNPPVNCRQLPRGPPSQVP PRIHLSPKYSPSPEASAPDLQKKGNL QAPRRPGEVLETPRKPESSCMKPFP* REIKPLPPPRLTPSVHSMVL
3780	9277	A	4055	445	448	IS*HCDASASIFRKKQRKQINKHPTL ASRVLGLAMEMQDETWCSGQSET VN*SQTAQNHPQPGS*PAGVCLWV ASSQHFTPQPLKKKPNPDSAKLNSA SDSLTEVILCKIFSAWQTDK
3781	9278	A	4056	3	284	CLSLLSSWDYKCLPPRLGYFLYF** RRGFTVLARMVSISRMVSISRMVSIS *RRDPPASASQNAGITGVSHCARPK EQKLFYPEVSCLYLGLY
3782	9279	A	4057	428	636	DYHIVSLLHLF*FLETGSHSVTQAGI QWCDHSSL*PRTPGLKQSSCLSLPE* LGLQE*VTVPGSYSLFF
3783	9280	A	4058	2	113	FFGRDGVSLCCPDWS*TPGLKGSSC LGLPKCWDYRRE
3784	9281	A	4060	36	359	RSGVQNGFHQAEVLSVRLCFSTEAL GQNPMPFPAPPGATSSPGPRPSCHL HSQKL/TLLHAQTLVTPLPL*GLGLS AWRTLAGGAPGLHPFTTHALSTPET IPGAYRRT
3785	.9282	A	4061	17	168	APGMVSGVLSACVVNGWSPGAPPA SVLQA/PQT*PF*SRPHVTSQPLLKA PH
3786	9283	A	4062	2	375	FFFFFENHTNLLSYSSRGSGVQNGF HQPEVLSVRLCFSTEALGQNPMPFP APPGATSSPGPRPSCHLHSQKLPLLH AQTLVTPLPL*WPPWITQGPPQPST GHLPTTEILKLKHRRRVPFCHAR

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3787	9284	A	4063	309	620	
3788	9285	A	4064	3	218	LRQSYSVTQAGVQWRNLGSLQPLP PGFKRFSCLSLRKS*DYRRPRLPNFC ILVKTGVHPCWSGWSQTLDLR
3789	9286	A	4065	1	170	NPKATPPQIVNGDQYCGDYELFVE AVEQNTLQEFLKLA*VKPVQSSPAG LHHHTPL
3790	9287	A	4066	29	483	RRLPAVQLPLTAALCPPARLSTPSM SGPARSTARRATGFREIKVPSKSEVT RIL\EGKRIQYQLVDISQDNALRDEM RALAEQPQGHPTPDLSTGDQYCGD Y/DASFVEAVEQNTVAG\FPGSLGL KFKPCSRVSPCWDSHHQHSPPAFQP GQ
3791	9288	C	4067	33	236	MRHHAWLIFVLLVETGFHHVGQAG LEHLISGGPPTSASQSAGITGVSHHA WPIYLFILLSGPSRLCF*
3792	9289	A	4068	1	205	AIGTDKGTRWPSEDDPGNLPEIFLFI LGPTADYV*RERQRSIELESFYRRV WGSPGGEGTGDLDEFDF
3793	9290	A	4070	2	44	LSSWDYRHVPPRLANFCIFSRDGGF TMLARLVLNS*PQVIHPPQPP*VL*L QACATTPG
3794	9291	A	4071	173	369	CSTLI*IRKVWLGAVAHAYNPNTLR GRGGRIA*GQVFKTSLGNNVKTCLF LPSPHNQQSLSGFLL
3795	9292	A	4072	1	336	
3796	9293	A	4073	1	200	
3797	9294	A	4074	11	392	
3798	9295	A	4075	1	191	
3799	9296	A	4076	84	264	
3800	9297	A	4077	2	446	DSARNSRVDGCE/IDRQKGTNDSLM MLMRELEDRFASEASGYQDNIARL EEEIRHLKDEMARHLREYQDLLNV KMALDVEIATYRKLLEGEESRINLPI QTYSALNF\RETSPEQRGSEVHTKK TVMIKTIETRDGEVVSEATQQQHEV L
3801	9298	A	4080	3	196	SRAKGPKNYNFGQGPPTKVKGPLA SPFFPLLPPFPRPPWFPFPPF*NPIFPW W*KGPKKPFLLN
3802	9299	A	4081	1	187	SIRLFFFCFFF*AETGFRHIGQAGFGL LTSSVPPALASQSAGIIGVSHRARPC SSLIVLHL
3803	9300	A	4082	156	326	KLEICRRARVSLKIGFIRPGTVAHAY NPSTLEGRGRQIT*DQEFETSLANM VKPCLY
3804	9301	A	4083	3	448	
3805	9302	A	4084	1	4249	AAATIRYLKTTMAWKTLPIYLLLLL SVFVIQQVSSQDLSSCAGRCGEGYS RDATCNCDYNCQHYMECCPDFKR VCTAELSCKGRCFESFERGRECDCD AQCKKYDKCCPDYESFCAEVHNPT SPPSSKKAPPPSGASQTIKSTTKRSP KPPNKKKTKKVIESEEITEEHSVSEN QESSSSSSSSSSSSTIWKIKSSKNSAA NRELQKKLKVKDNKKNRTKKKPTP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KPPVVDEAGSGLDNGDFKVTTPDT STTQHNKVSTSPKITTAKPINRPSL PPNSDTSKETSLTVNKETTVETKET TTTNKQTSTDGKEKTTSAKETQSIE KTSAKDLAPTSKVLAKPTPKAETTT KGPALTTPKEPTPTTPKEPASTTPKE PTPTTIKSAPTTPKEPAPTTTKSAPTT PKEPAPTTTKEPAPTTPKEPAPTTTK EPAPTTTKSAPTTPKEPAPTTPKKPA PTTPKEPAPTTPKEPTPTTPKEPAPT TKEPAPTTPKEPAPTAPKKPAPTTPK EPAPTTPKEPAPTTTKEPSPTTPKEP APTTTKSAPTTTKEPAPTTTKSAPTT PKEPSPTTTKEPAPTTPKEPAPTTPK KPAPTTPKEPAPTTPKEPAPTTTKKP APTAPKEPAPTTPKETAPTTPKKLTP TTPEKLAPTTPEKPAPTTPEELAPTT PEEPTPTTPEEPAPTTPKAAAPNTPK EPAPTTPKEPAPTTPKEPAPTTPKET APTTPKGTAPTTLKEPAPTTPKKPAP KELAPTTTKEPTSTTSDKPAPTTPKG TAPTTPKEPAPTTPKEPAPTTPKGTA PTTLKEPAPTTPKKPAPKELAPTTTK GPTSTTSDKPAPTTPKETAPTTPKEP APTTPKKPAPTTPETPPPTTSEVSTPT TTKEPTTIHKSPDESTPELSAEPTPK ALENSPKEPGVPTTKTPAATKPEMT TTAKDKTTERDLRTTPETTTAAPKM TKETATTTEKTTESKITATTTQVTST TTQDTTPFKITTLKTTTLAPKVTTTK KTITTTEIMNKPEETAKPKDRATNS KATTPKPQKPTKAPKKPTSTKKPKT MPRVRKPKTTPTPRKMTSTMPELNP TSRIAEAMLQTTTRPNQTPNSKLVE VNPKSEDAGGAEGETPHMLLRPHV FMPEVTPDMDYLPRVPNQGIIINPM LSDETNICNGKPVDGLTTLRNGTLV AFRGHYFWMLSPFSPPSPARRITEV WGIPSPIDTVFTRCNCEGKTFFFKDS QYWRFTNDIKDAGYPKPIFKGFGGL TGQIVAALSTAKYKNWPESVYFFK RGGSIQQYIYKQEPVQKCPGRRPAL NYPVYGEMTQVRRRRFERAIGPSQT HTIRIQYSPARLAYQDKGVLHNEVK VSILWK\GLPNV\VTSAISLPNIRKPD GYDYYAFS\KDQYYNIDVPSRTARA ITTRSGQTLSKVWYNCP
3806	9303	C	4085	258	362	MFYRNLMKVRAELNCSAIILIEIKA KVLTLFHSN*
3807	9304	A	4086	2	236	QSYNSDSLFFLRRSFALVTQAGVQ WRDLGSLQLPSPGFK*FSCLSLPSS WVYRCPPPDPANFLVLVETGFHHV GQGWS
3808	9305	A	4087	224	464	KIFLFFFFFKKRQGLTLSCRLDCSVQ *HNHYPLQSRTPELKQSSCLSHPKY WD*RHEPLCLAPKKEDTLQEQLEIR LLIY
3809	9306	A	4088	129	315	ILKILWIFRIFLLSIKCFF*TNMHVCV

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						SCLFIFLTVSFIEQTF*ISFFYASWIML LMSFFF
3810	9307	A	4089	1	190	FFF*IGPHSVAQAGVRWCDLGSCSL NLPGSSDPPASASQVAGTTGVHYYT QLIFKFFIEMRAP
3811	9308	A	4090	1	5229	
3812	9309	A	4091	1	7044	
3813	9310	A	4092	170	422	
3814	9311	A	4093	1	3230	
3815	9312	A	4094	3	151	DTATCCAKWNTEDKVSHVSTGGG AS*ELLEGKALPGVDATSTIYYFPAF
3816	9313	A	4095	2	1446	SLRSARRQSAPSLTESPTSLPSCISK MSLSNKLTLDKLDVKGKRVVMRV DFNVPMKNNQITNNQRIKAAVPSIK FCLDNGAKSVVLMSHLGRPDGVPM PDKYSLEPVAVELKSLLGKDVLFLK DCVGPEVEKACANPAAGSVILLENL RFHVEEEGKGKDASGNKVKAEPAK IEAFRASLSKLGDVYVNDAFGTAHR AHSSMVGVNLPQKAGGFLMKKEL NYFAKALESPERPFLAILGGAKVAD KIQLINNMLDKVNEMIIGGGMAFTF LKVLNNMEIGTSLFDEEGAKIVKDL MSKAEKNGVKITLPVDFVTADKFD ENAKTGQSTWA\SGITPG\WMGLDC CPESS\RKYAE\AVTRAKQMVWNGP V\GYFE\WEAFA\RGTKALMDEV\VK A\TSRGLPSPS*GGWRPLPTCCAQM ETREDKSQPM*ATGGWCPVWQLLE G*SPFLGVDALSQYLGTFPALLSPC AQPPKVNLGIFLHLPLGH
3817	9314	A	4096	1	747	MDSSRARQQLRRRFLLLPDAEAQL DREGDAGPETSTAVEKKEKPLPRLN IHSGFWILASIVVTYYVDFFKTLKEN FHTSRSPESPAPRRGGVRASVPQKL AEMLSSQYGLIVFVAGLLLLLAWA VHAAGVSKSDLLCFLTALMLLQL/P VDAVVRGPQLRAPPPLPPQGHARG CRLAARQRPPTVSTGRGEHVDSPPP AQRRSYLPLRLRGAEFASEPPSAPA HR\ATPPPVEVTPTEAGRRFRQAKG ALS
3818	9315	A	4097	1103	1295	EQEGTGLERRRGSPMSKDWPPPHL TPPQGPCGIPVHSLSPPSFS\PGPRNS K*ARRSTAPVDCK
3819	9316	A	4098	1	1302	MVAGSDNYHEVSLHDGVIGARGCP PPSPSARGARSPRPPGGCARQPTEA GRDAEQPVWADRVRGGAAAAAGL GRARRGLAESDLLCFLTALMLLQM LWYVGRSSAHRRLFRLKDTHAGAG WLHRLLWIPPAFGCRPEYDNGLEEI VFGFEPWIIVVNLAMAFSIFYAMHA AASLFEVYSGISETSVLGDWSKPSTF DSKASGLRHLKTSKGKSSLVNASIP TPPSPFRPSQPSEPASQPAKPAKPAK PVSQPSQPSQT\PGKPAKPAKPPKPA KPPASQASQASQPGMPAKPAKPAS

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						K/PKPGMPAKPARQPSQPAKTAKPA NQPSQSASQASQPASQPSRPACQPT KSARQPRQPSLPAAKRANATYQRS HSASQDRHASEPTSQPSSQHSAARP AATSQPDSRAANQSAVEQARQPSA KHSGKQQADSEAAAGS
3820	9317	A	4099	684	902	
3821	9318	A	4100	143	551	TNEFPFHSRSPPQIQTS*AHFPHLITD PDLLSPLSPSHHRSRPPEPTSPISPQIQ TC*AHFPHLITDPDLLSPLSPSHHRS RPPEPTFPISSPVISWAPAISFPNCCC KQTATDSSGFHFCLIVLIAKSPKRISP G
3822	9319	A	4101	14	209	ASFKVWLIWE*RPWHGTYPSCKNW GKFASGSVTIWFKLPSGPLALSGIL MRLLLLSLSLHENSVS
3823	9320	A	4102	126	265	
3824	9321	A	4103	74	196	NLGMLAHAYNSRNLGGQVRTII*G QKFETSHENISRPCLV
3825	9322	A	4104	1	217	NIYMFLICFVLIFNFLNELIT*KHIVIF ICWIILSLLLLTLH*FWCHKFHVSW NLEFCIFYFGFKIKLDTFT
3826	9323	A	4105	3	268	DRVLLCCPGWSAVSQS*LTAPQTPG FK*SSHLSLPSSWDYRHIPPHLAKK QKYFK*RWSLPVLPRLV*NSWAQAI FPCQPPKGLGLQA
3827	9324	A	4106	3	263	DSLALSLRLECSGVISAHCNLCFLGS NNSPAAASRVAGTTGACH*DWLIFE FLVETGFHHIGQAGLELLTEVICLP WPPKVLGLQM
3828	9325	A	4107	22	208	SFSIQGPLLLKPNS*PGVVAHSYNPS TSGGQGRCIT*GQEFESSLVHMAKP HLYQKIQKICR
3829	9326	A	4108	122	339	EKGFWFCAQGGKNLPGGNSLEPSA SGLKEIFGLNLLNNWE*RGGPKTPG NFWIWKKGGV*PLWPGWG*NPGL
3830	9327	A	4109	2	210	KEKIFPSPGFKHPPPPPF*KTPLKGK RIFFSPPRKNWPPQRIFKKAPPSSSSS SSSSSSSSAQI*SFNSP
3831	9328	A	4110	3	76	ATSESLDVMASQKR*SRSGSPMARR
3832	9329	B	4111	1	2142	MGGAGSPQVILVSHTPQSASAACEE IAYQVAGVSGNLAPGNQPEKEGRA HQCLECDRAFSSAAVLMHHSKEVH GRERIHGCPVCRKAFKRATHLKEH MQTHQAGPSLSSQKPRVFKCDTCE KAFAKPSQLERHSRIHTGERPFHCT LCEKAFNQKSALQVHMKKHTGERP YKCAYCVMGFTQKSNMKLHMKRA HSYAVAVAMGGTAQCPPGATACL GTAICPSGLRAQRPSNLSVPEAAKP KSGRNRKIEAPTWALSTSKDPQTEG LRNPQTCVQIRSNPFCAFAQGFSLIS ELRTLNCFVGLCDSQSGKQQLGFYS GQPATEAWQKYSLAVCILRSEQEIS ATRLGLKNTNVNKLDGGCGAWNF LGGMSEHNSPPSGRAILLPVVFTEV FPGPWTPEQGSHICRMNLAPTFQAF

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						LPKTGFPIDPQELLQGPIERTIWPGT VYTFRSAIVTARAVWVRPRMDRRA DLSSATQSASAEKFGGRVSAGHCA LPLPARPVTASVYGRLARLRGCLED SYPSALSAQVFLDSPAVGCGLETRL FIEAALGPPCRATVTSRGHLLDISIT KSPGRPCFLSVCLHGSDQQKRKGA AATAKRKSKGGGVNVEGRLCTWPP EDPPKSWSLAFGPLQEKTTELNLHP RCWARCLSHWELPPGPRGRAQAPD WTGSKSFREQLLTFTLWGVQEKISK HQANQGKEAPAYTGLEDSDPGGLC AV*
3833	9330	A	4112	1	551	
3834	9331	A	4113	3	288	CIGLGVVAHACGPGTLGGRGGRIT* AREFGTSLGNIARSHLYKKRKNSES QMSLHLLTLDLTPYISAAFASPVDA DTQLSACTFQLKETPMPSF
3835	9332	A	4114	3	344	VQYYGPAT*VQDGS*GYRTHMYMI NQIIWLQAVLKIITNKTGRALTILTQ QETQMRNAIYQNRLALDYLLAAEG EVCRKFNLINCCLHIDNQGQVFEDI VRDMTKLAHVPMQV
3836	9333	A	4115	6	185	LAGHDRVRL*SQLFRRLRREDCLSS GGRGCSEP*SHHHTPVWKTKLGPV SKEKKYNQIV
3837	9334	A	4116	1	176	QSIFQICIFFKFTVYMFKTFLKFQTV FLCGRCWFL*KGLIIFFTLYFKTFHH IVRGIK
3838	9335	A	4117	1	312	GGEKNQDFTFKMESPSDSAVVLPST PQASCLSLPSN*DYRHPPPCPANFCI FSRDWVSTHVGPGWSRTPDPQVIH RLGLPKTIRGSEEGIPDEYQLKGTLI YKL
3839	9336	A	4118	1	112	GKTFKQKQKQEQKKQK*ELK*KAM GKGPLAAGEIKKS
3840	9337	A	4119	3	355	SQSTKNLPSLARDMDIQIQEAQRSP KRSPPRHIIFELTKVKDKEKNPKVPV EKHQVIYKGIFIRITAETSQARKKW DDISKFLKEKKKYRSKILCTANQSIR N*VEIASHSGSCL*SMILTA*PATVA HAYNP
3841	9338	B	4120	638	3862	MKGTCVIAWLFSSLGLWRLAHPEA QGTTQCQRTEHPVISYKEIGPWLRE FRAKNAADFSQLTFDPGQKELVVG ARNYLFRLQLEDLSLIQAVEWECDE ATKKACYSKGKSKEECQNYIRVLL VGGDRLFTCGTNAFTPVCTNRSLSN LAEIHDQISGMARCPYSPQHNSTAL LTAGGELYAATAMDFPGRDPAIYR SLGILPPLRTAQYNSKWLNEPNFVS SYDIGNFTYFFFRENAVEHDCGKTV FSRAARVCKNDIGGRFLLEDTWTTF MKARLNCSRPGEVPFYYNELQSTFF LPELDLIYGIFTTNVNSIAASAVCVF NLSAIAQAFSGPFKYQENSRSAWLP YPNPNPHFQCGTVDQGLYVNLTER

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						NLQDAQKFILVHEVVQPVTTVPSFM EDNSRFSHVAVDVVQGREALVHIIY LATDYGTIKKVRVPLNQTSSSCLLE EIELFPERRREPIRSLQILHSQSVLFV GLREHVVKIPLKRCQFYRTRSTCIG AQDPYCGWDVVMKKCTSLEESLS MTQWEQSISACPTRNLTVDGHFGV WSPWTPCTHTDGSAVGSCLCRTRS CDSPAPQCGGWQCEGPGMEIANCS RNGGWTPWTSWSPCSTTCGIGFQV RQRSCSNPTPRHGGRVCVGQNREE RYCNEHLLCPPHMFWTGWGPWER CTAQCGGGIQARRRICENGPDCAGC NVEYQSCNTNPCPELKKTTPWTPW TPVNISDNGDHYEQRFRYTCKARL ADPNLLEVGRQRIEMRYCSSDGTSG CSTDGLSGDFLRAGRYSAHTVNGA WSAWTSWSQCSRDCSRGIRNRKRV CNNPEPKYGGMPCLGPSLEYQECN TLPCPVDGVWSCWSPWTKCSATCG GGHYMRTRSCSNPAPAYGGDICLG LHTEEALCNTQPCPESWSEWSDWS ECEASGVQVRARQCILLFPMGSQCS GNTTESRPCVFDSNFIPEVSVARSSS VEEKRCGEFNMFHMIAVGLSSSILG CLLTLLVYTYCQRYQQQSHDATVI HPVSPAPLNTSITNHINKLDKYDSVE AIKAFNKNNLILEERNKYFNPHLTG KTYSNAYFTDLNNYDEY*
3842	9339	A	4121	3	124	NVNRPVSSNEIKIIIKSLPVKKSP*LN GFNAEFTKHVKNL
3843	9340	A	4122	1	197	GFKQLS*LSLPNSWDHRHTTTTPRE MGFHHVGQAGPELPISGDPPAPASQ SAGITGVSHRTRPRI
3844	9341	A	4123	1	268	QLYHLSLQSSRDHRCEPPRPANFLII CRDEVYVAQAGLKLPSSSDPPASAS KSAGSTGVSHCTQAKFYFF*NLMG EMRGKNNKHLTSFK
3845	9342	A	4124	3	301	TEEIHGVLSWNLVPDNYPPYYHPPP PSYIYGAQHLLRLFVKLPEILGKMT FSDKNLKALLKHFDLFLKHLAEYH DDFFPE*AYVAACEAHYCTHNPRSI
3846	9343	A	4126	2	214	FFFFKEMGSHYVA*AAVKWLFTGA IITL*SLKLLDSNNTPALSECKLIITQ EASVLKIKKVEIKKTKNRN
3847	9344	A	4127	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLVT LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
3848	9345	A	4128	2	253	
3849	9346	B	4129	317	683	AHKLRVDPVNFKLLSHCLLVTLAA HLPAEFTPAVHASLDKFLASVMHR ADLQIPLSWSLATGCQKLIEVDDER KLRTFY*
3850	9347	A	4130	1	82	VDGWVDGWVDG*MDR*VGRWID

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GWVDG
3851	9348	A	4131	1	240	ASTFFFFSIDRVLLCCPGWTRTPGFI*SSCFGLPKCWDYRSEPPCLATFFFIKKKYKEEHFILILCQIVNMILILYQPTQ
3852	9349	A	4132	3	180	REPPLPAANFVFFVEMRSHHVRQAGPEPPSSSDLPASASQSAGITGVHCHAWP*YTYL
3853	9350	A	4133	2	238	SPCAGILEDDRADYQGTRKTSEYSSVTP*EACHT*EGPIAFISWP*KVPIQLTFNERNRARGFQVPYGTYDRGLPGTH
3854	9351	A	4134	7	259	IVTAALFTLAPNQK*SKYPSSGKLINKFWYIYKME*TSISNKQVSTTYSMQAWVNLKSITLS*RHKGVYII*SHLYDILEKTEL
3855	9352	A	4135	141	309	AFDEAIAKLYSVNE*SYKGSTVIMQLVRVNLAVSATSTGFIVSFVFTYPIIPCYLQ
3856	9353	A	4136	113	205	HNLLMLFDLCLLYWL*LIFLIHELAENLLN
3857	9354	A	4137	3	215	FETGSCSVTQAGVHWRDHSSLQP*SLGFKQPSNLSLPSSWDYRCTPPHLANLCIFCKDRVTSYCPGWHPV
3858	9355	A	4138	3	386	
3859	9356	A	4139	1	255	IRLMKEGRMKGQAFIGLPNEKAAAKALKEANGYVLFGKPMVVQFARSARPKQDPKEG*RKKRTWLFNKVGKWELAPKPMGLDFSL
3860	9357	A	4140	78	153	
3861	9358	A	4141	1	293	LRLPGSSHSPASVS*VAGIAGACHHAWPNFCVFSRDQGFTHVGRAGLGAPDPLDPALPWPSPKVMGFTRCEAHPCPSPRMRFLKYVSVPVSMVGRPE
3862	9359	A	4142	3	48	PLPRKSVEPGGGTKYKTEQKKRQERRDRGSK*RKQQKAATSEEQQRK*AKTQEDGGTKRSPDGEEDPEKKIHRNREGTRKKGQDPRNGVNNKNREKEQN*RTHTS*SQKVRRTRRGNEV
3863	9360	A	4143	1	276	GTRDSV*GGLKLIPIFLMDFWKEPLGPALAHELQYPGRD*SSDIWIRTAASLHTLPIVGPHLLGDLASFCTLLTPDPCQHVPRSRADTVEMG
3864	9361	A	4144	1	154	LVWS*EASKIPGGAEAAHPPTTF
3865	9362	A	4145	2	231	FFFESGSRSVTQAGVQ*HSLGSLQPLPPRFK*FSCLSLPSSWDYTHVPTRPANFCIFSGDGVSSCWPGWSRTPNLR
3866	9363	A	4146	1	303	GTRGSVKEGAKYTSHRDMGLSTFDRDADQWKENCANVYG*GCRYNNCQAANLNGIYYPGGSYDPRNNSAYETDNGVVWVSFTGAHYSLRAARMKIRPLVTQ
3867	9364	A	4147	3	372	HAGLGAHPLHHPVIQQEGFLPAPRGFGYRSEVD*IRIPAESTGQNSQCQLRK*KDDSYFHCGYFCGCVCTCRGRLQSSTSHQCQAAL*LLLPVCLTMLRCISSLIYT*NLKTVHSVRLNFIYN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3868	9365	A	4148	2	98	RRPFFFFFFASCI*NLISPNVQLSNFT CILRN
3869	9366	A	4149	1	230	SGRPFLFFFQGKERVYFIPVVVLFYT VVVQ*LRKNVVRWQKTMEPPRSW LMQLGHTEEGPGYPLLGETETKLFR TA
3870	9367	A	4150	1034	2354	DRVLAPVAQTGVQWHDLSSLQPPP PGFKRFFCLSLPSSWDYRRPP*RPAN FC*FLVETGFRHVGQAGLGLLTSGD PPASASQSSRITGVSHRARTMGLSR ALYRIPALKVWLLINVELKKQMMA HVDVTCLINKSPSLTRPMGKRLSAE TGKGQKEKQKQTGAGCAVLPSRGF PPKAHHGRQPLTLAPSPPPRTFSPSP PHTHTHTHTCSPICPRQSRSFQGPR MPDPDPGDATCGAGPGGSAPARAA GPRSAPRRAKARVQARVQARAQAR WVRALTLLAAHPRLQPVPARIARR AAQSSSSPPPATPAKSPPPEASGAAA PPALGLERFPGASPNHLTRSTCALR HVGAGGAALGGPGAPRLPHRLEVG REEGRGRRGDGLGHGGCVEPAWEP GWRLPSTIKLFIKSKVSSEALEMPFL CICEHLLSYTYSRKHRNVI
3871	9368	A	4151	387	478	
3872	9369	A	4152	757	1477	HKENRNSLELRQNQSSPIWALPLHG LERKGLGRDHSSPHLPLLPSERL*K ASASQGPEWCCPSPRAAGPESGRCD QLWESPMASATWKPYRPQPSRSPQ RQRVVLPPLVKGKTPPLFKLLQESV PGDLLPGELSL*PWEKPI*NNFAFNF SQQCKGMFKFPQFRSLARGSNPTSL TGVGPLPLPREFPGEEREGAPQIFKQ NTANGLGPSA*MRAGTAQGCWES* GGNTAPGPGAVNTAN
3873	9370	A	4153	32	255	SRRHDSLHRVTFCISDPHYRKWTNP DGTTSKIFGFVAKKPASPWENVCHL FAKLDPY*PAGAIVTFITNVPTAP
3874	9371	A	4154	1	265	CDTVLLCHPGWSAVAQSQLTTTSA SQIKRFSCLNLPSSQNTRRASPHPAN FFYF**R*GFTMLVRLVSNSCPQVIH PPLPPKVLGLQA
3875	9372	A	4155	92	333	FLSFFFF*MGCHSVTQCGVKWHDLS SLQPPHLTFKWFSRLSLLSGWDYRC LAQHQASCCIFSRDGISPF*PCWYQT PDLR
3876	9373	A	4156	16	181	ICSLPSTVDVIEFLDYYVKVSLKL*SI IKICDSDKHTHIHTYGYVYIFSPPGK PV
3877	9374	A	4157	1	355	TVSLSCSVAQAGVQWHNLGSLQPL PPGFK*FSCLSLPSSWDHRCPPPCLA NFCIFL*RWGFARFCHVGEAGLELL TSSDLHTSDSQSAGIIGTSHHAWPH LLVLTCVCAHTLFRHFYL
3878	9375	A	4158	1	194	FFFFFTISYIFIYTLTTCWEFKQLAGN I/HL*GTVAFFYLKLLKLQDRLTNSF SSATTNVLAENS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3879	9376	A	4159	112	270	ILGNSLFKNYK*YLSPAAVTHACNP NTLGGQGGPVT*AQEFETSLGNIVR PCL
3880	9377	A	4160	1	211	RFSCLSLLSS*DYRRVPPRPAIFVFL VETRFHYVGQDGLDFLTSCSARLYL PKCRDYRRELLCPAPASLL
3881	9378	A	4161	2	253	ETDSCSVAQTRVQWYDLGSLQQPP PRFKRFSCLSLPNSWDYKCVPPTPI* FFLFLVEMEFHCAGQADLELLGSGD PPASASPK
3882	9379	A	4162	198	276	KPFMAQCSF*IYEAIFSCTSSEIRY
3883	9380	A	4163	3	193	HFGRPRRADCLRSSV*DQPGQHGET PSTKNTKISQAWWWVPVVPTT*EA EAGESLEPGGQRLQ
3884	9381	A	4164	2	515	DTEKMSPWDMELIPNNAVFPEELG TRVPLTDGECKTLIYKPLDGEWGTN PRDEECERIVAGINQVMTLDIASTFV APVDLQAYPMYCTGVAYPTDLSSI KQRLENRFYRRVSSLMWEVRYIEH NTRTFNEP*KPNGRPAKSGTDLLLH FIKDQTCYNIIPLYNSMKKKVLS
3885	9382	A	4165	3	418	HEADKTNVVTGKTEVGAHAGEYG AQALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKVADALTNAVTRIK EMRNALCTLSDLYAHKLLGDSCTL *LLSHCMLVTLAN*PSSEFTPVAHTL VAKILAFVSTELTSKY
3886	9383	A	4166	1	191	CLETECRYVSQAGMQWHYPG*LQP *PPGYKLSSHLSLPSSWDYRHVPEH PTNFVYFFVERKSH
3887	9384	A	4167	3160	3732	
3888	9385	A	4168	2	326	PRSGSESFSCQLSPFFFFFGDRVSLC GPG*SAVV*LQLM*PGPPKLKQSSC LCLPSSWDHRWAAPHLA*FFKFFFI ETGSYHLPQLVSNPWAQASLLPWP PKVLGLQV
3889	9386	A	4169	2	163	LIFFVFIVGTGFHHVGQAGLECLTSS DPSASASQSAGITGVNHHTRPPSAF GC*T*GTGFHHVGQAGLECLTSSDP SASASQSAGITGVNHHTRPPSAFGC
3890	9387	A	4170	126	348	HISIFETGSYSVTQAGAQWLDHGSL QP*PPGLK*SSCLSLPSSWDYRHMPP CPANFYIFCRDGVSPRCSGCNF
3891	9388	A	4171	1659	1970	MLKGGAKIRSRRKTGVSHSLHSDL NFFFFWDKSIALSHRLEYNGAISAH CNLRLLGSSDSPASAS*VARITGMR HHTQLILVFFSRNGVLPCWPGWSRT PDLR
3892	9389	A	4172	153	278	MRPDTVAHTCNPSTLGGQGGRIT*T HEFETSLGDMMKPYLYK
3893	9390	A	4173	3	254	LQYLVFISSKAWPS*KLEDGET*SA GENNNYNTIL*LDLFSHREGKWSKI PYV*AFFALQNNRKLCQQCIIDLALI AVISSQT
3894	9391	A	4174	3	225	SLTHLTATSILLK*FSCLGLPSSWDH RCPPPRLANFFAFLVETDFTMLARL V*NS*PEVIRSPRPSKVLGLRA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3895	9392	A	4175	1	344	GGALSGGTPGFSPSPPGKTAAPGQS GNPPGGF*RVPSPGGSQRGGFPGNT PAPGPLPSSSSSSKGGFGDCTPRDKS RKGGKPPFS*GGFFPQGSAVPKHLA APTNRYTSFHPQK
3896	9393	A	4176	2	201	QPGQYGKHPVLIKNSKIKPFWGDPP VVPNAREG*A*KMVEPGKVRVQSA QIKALEFNLGPKKKVPF
3897	9394	A	4177	39	225	KSIQSYAI*YNVTCGFFKSALNGVG SVAFCSHHAEHFLGFVFINHEKSFQ FCQMLLLCMTR
3898	9395	A	4178	322	451	INSTDWAPWLTLVISALWEAEAA/G SRGQEIETILANTVKPRLY
3899	9396	A	4179	234	383	
3900	9397	A	4180	86	216	KQTLGQAWWLTPIIPALWEAEVGR S*DQEIETILPNTVKPHRY
3901	9398	A	4181	1	4123	MEEVEEDRFKENLEGALAGQLLGD EATQALQVLAVELDVVVPGALHPQ RLHRLGAALVERQPVREVDHLVLP AVDDEHGRRDLGHLLDVREGVEA VGLLGVAEGDAHARGERRVQHHR GTLVARGQVHGGHRADALPVQDD AVRADAVPGGAGAGSAAASNARA PFPPAGVPGPSSGCDPPVSPLSQVSA HWELCGPHILNASYLPARVRKPFLV HWPGQRTLFLPAALAHPLGHEEFR QLCPQMSPPNFGLSESPRPVRCQCN PGQHRGWWLRRWHPLPPAPSLGSG QVLGHLSTTSSHPGAPSPPGHWCAA PDPADPAPVTRPPRAQSQARGTHLP PCPCRDPTTLLPHALGSDPRQTPSC KAGAWAGRSPQLPPGCHHSNERDT SPVEALGTLWPPPHGSGPRFLQDKG AAGQMAEQTELRAGHGRMAKLRS HRASWASPPDLDAAASPHLAPSAA SADGLPATRAQTPRPPPTPSRQAELP PGSPSPGAQGLPGGVDVGIEVPLGR PARAGTVAGGVVGEDVAVEAGAQ ANVEAAHLAQVHGIAVREEDRVPG TRHAANIHAGDTVAAGALGGEDLD GVQLALAVLEVGTLRQGFWWTLR GTDVETYPFSAPRAASHGVGRHEEL PDPTGPCGGRLLSLTIHGVTIRYHAL LWARGPIMSKSQVLGEWEPVQGGK SSENDKWTMSDPGAEAPTCSRAAS GVDKEQQGRWQGLWNSHIKPLKIR MVKQNNIIPGETQILLRFTGWESKV NAKKQLPVGIKCEPMDQENEQTGG HETDGHRIVSVLIHFPLISILSYATW GLSLLECIPGSPVCTLLVRFSNVGTR WSLEVRGSPCGFGSNKVCGVMTPEI KMVCVCEGKAGKAVGSGGVEGTK EVSTGNAEGPVRHEAVDGGVHLAF ALLQGLLWSLLLGPPGLAGWGGGE LDAVPDSTSSATNVSMVVSAGPWS SEKAEMNILEINEKLRPQLAENKQQ FRNLKERCFLTQLAGFLANRQKKY KYEECKDLIKFMLRNERQFKEEKLA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EQLKQAEELRQYKVLVHSQERELT QLREKLREGRDASRSLNEHLQALLT PDEPDKSQGQDLQEQLAEG\LDWH STLSKSSAQKMTKMRMKMFK/CEE DEKVLESSAPREVQKAEESKVPEDS LEECAITCSNSHGPCDSIQPHKNIKIT FEEDKVNSSLVVDRESSHDGCQ/EC SKHSPSPWPHLFCHKRQHGG/DQPA LCPARRQR*TF*KSMRNCA/HQLAE KKQQFRSLKEKCFVTQVACFLAKQ QNKYKYEECKDLIKSMLRNERQFK EEKLAEQLKQAEELRQYKVLVHSQ ERELTQLREKLREGRDASRSLNEHL QALLTPDEPDKSQGQDLQEQLAEG CRLAQHLVQKLSPENDEDEDEDVQ VEEDEKVLESSAPREVQKAEESKVP EDSLEECAITCSNSHGPCDSIQPHKN IKITFEEDKVNSSLVVDRESSHDGC QDALNILPVPGPTSSATNVSMVVSA GPLSSEKAEMNILEINEKLCPQLAEK KQQFRSLKEKCFVTQVACFLAKQQ NKYKYEECKDLIKSMLRNERQFKE EKLAEQLKQAEELRQYKVLVHSQE RELTQLREKLREGRDASRSLNEHLQ ALLTPDEPDKSQGQDLQEQLAEGC RLAQHLVQKLSP
3902	9399	B	4182	1	799	MLQIPKQQQNEKYQVPQFDQSTIKN IESAKGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDADDTSIYM FYQKVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHYGKQSLTTAQI HFPLISILSYATWGLSLLECIPGSPVC TLLVRFSNGGPPMDPGSERKGFCRF RNHHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHPGAQ YANRLSPRVGRFINAAGTTX*
3903	9400	A	4183	260	387	REVGRVRWLTPVIPARWEAEVGRS *GQEIKTILANTVKPRLY
3904	9401	A	4184	1212	1442	
3905	9402	A	4185	3844	4180	KYKKCVGCGGRSL*S*LLRRLRQEN RLSPGGGDCSEPRSSHCTPAWVTER /GDSVSKKKKKNLLTWLVNKLCGP CRAWWLTPVIPALWEAEAGRSRGQ EIETILANTVKPRLY
3906	9403	A	4186	8	385	
3907	9404	A	4187	2	284	
3908	9405	A	4188	1477	1697	
3909	9406	A	4189	17	385	
3910	9407	A	4190	1	837	GKVVLELERFLPQPFTGEIRGMCDF MNLSLADCLLVNLAYESSVFCTSIV AQDSRGHIYHGRNLDYAFGNVLRK LTVDVQFLKNGQIAFTGTTFIGYVG LWTGQSPHKFTVSGDERDKGWWW ENAIAALFRRHIPVSWLIRATLSESE NFEAAVGKLAKSPLI\ADVNYIAGG TCPREGVVVTRNRDGPGDIGPLNPL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NGAWLRVETDYYHWKPAPKEDDR RTSA\IKALNATGQANLKLEALFQIL TVVPVYNNLTIYTTAMSAGSPYKY MTRIRNPS
3911	9408	A	4191	653	727	
3912	9409	A	4192	26	161	
3913	9410	A	4193	3	186	
3914	9411	A	4194	28	186	
3915	9412	A	4195	356	428	
3916	9413	C	4196	35	430	MKSCRXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXX XXSETNSWEATRKPNFSSNSESAFIS RSQGHKDAKKEFVPLXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXLQSHPLVR*
3917	9414	A	4197	213	394	
3918	9415	A	4198	28	123	
3919	9416	A	4199	1578	1835	SNKSLPHNCIPPQMRNYSRGNLLQY IDYVQLHRNLYAGEIYFHC*RKSAL CNSSWREGAVGCLPMDFPRLHLSL SPSSLHCRNKP
3920	9417	A	4200	213	305	
3921	9418	A	4201	1715	1850	
3922	9419	A	4202	4016	4315	
3923	9420	A	4203	28	239	
3924	9421	A	4204	7	216	
3925	9422	A	4205	1	576	
3926	9423	A	4206	1	500	
3927	9424	A	4207	1	1266	
3928	9425	A	4208	1	162	
3929	9426	A	4209	1	229	
3930	9427	A	4210	197	416	
3931	9428	A	4211	1	131	
3932	9429	A	4212	76	274	
3933	9430	A	4213	295	2530	RPATMAARPLPVSPARALLLALAG ALLAPCEARGVSLWNEGRADEVVS ASVRSGDLWIPVKSFDSKNHPEVLN IRLQRESKELIINLERNEGLIASSFTE THYLQDGTDVSLARNYTVILGHCY YHGHVRGYSDSAVSLSTCSGLRGLI VFENESYVLEPMKSATNRYKLFPA KKLKSVRGSCGSHHNTPNLAAKNV FPPPSQTWARRHKRETLKATKYVE LVIVADNREFQRQGKDLEKVKQRLI EIANHVDKFYRPLNIRIVLVGVEVW NDMDKCSVSQDPFTSLHEFLDWRK MKLLPRKSHDNAQLVSGVYFQGTT IGMAPIMSMCTADQSGGIVMDHSD NPLGAAVTLAHELGHNFGMNHDTL DRGCSCQMAVEKGGCIMNASTGYP FPMVFSSCSRKDLETSLEKGMGVCL FNLPEVRESFGGQKCGNRFVEEGEE CDCGEPEECMNRCCNATTCTLKPD AVCAHGLCCEDCQLKPAGTACRDS SNSCDLPEFCTGASPHCPANVYLHD GHSCQDVDGYCYNGICQTHEQQCV TLWGPGAKPAPGICFERVNSAGDPY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNCGKVSKSSFAKCEMRDAKCGKI QCQGGASRPVIGTNAVSIETNIPLQQ GGRILCRGTHVYLGDDMPDPGLVL AGTKCADGKICLNRQCQNISVFGV HECAMQCHGRGVCNNRKNCHCEA HWAPPFCDKFGFGGSTDSGPIRQAG KEARQEAAESNRERGQGQ\EPLGSQ EHAST\ASLTLI
3934	9431	A	4217	2	119	
3935	9432	A	4218	2	147	
3936	9433	A	4219	10	216	
3937	9434	A	4220	245	455	
3938	9435	A	4221	1	2867	MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEEESNQATGTSRWDG VSKKAPRHHLSVPCTRPREARQEAE DSTSRLSAESGETDQDAGDVGPDPI PDSYYGLLGTLPCQEALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTIQLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIAK QAERVFPSNVICKTFHSMAYGHIGR KYQSKKKLNLFKLTPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPIWCKNSQGQRVMVEQSE KLNGVLEASRLWDNMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVIKDKFIRRW VHKEGFSGFKRYVTAAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPQLPHFRVESFSE DEWNLLYVAVTRAKKRLIMTKSLE NILTLAGEYFLQAELTSNV\LKTGV VR\CCVG\QCNNA/LSPVDTVLTMK KL\PITY*ATGK\ENKGGYLCHSCAE QQHRDPWRFLTASPEQVRAMEPHF GGTSYCPRHEALLFLVF
3939	9436	A	4222	57	302	
3940	9437	A	4223	1	550	DAHIIGRIESYSCKMAGDDKHMFK QFCQEGQPHVLEALSPPQTSGLSPS RLSKSQGGEEEGPLSDKCSRKTLFY LIATLNESFRPDYDFSTARSHEFSRE PSLKLVGLNAVNCSLFSAVREDFKD LKPQLWNAVGRGDLPGLKCDIYS\Y

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NPDLDSDPSREDGSLWSFNYFFYNK RLKRNRLL
3941	9438	A	4224	11	511	GRTRSIAGEETTQRPGPNCGGNCLC LHTLAINMRICYSQTTPFHPLRLKG QRWPF\FSSLELFPVGFPRAHLLVQS TLPKPRPERAFTAPSLFPVTLGFCLG RILCQRLLLCPSCLATALSINGYSRT QECQSWKGRDTGLHKGKLLEALG GTEGFGDRARAKIEDS
3942	9439	A	4225	1	279	
3943	9440	A	4226	1011	1322	
3944	9441	A	4227	3	468	TPLHVYNEVMSVGQKYGIRNAGYY ALRSLRIEKFFAFWGQDINNLT\TPL ECGRESRVKLEKGMDFIGRDALLQ QKQNGVYKRLTMFILDDHDSDLDL WPWWGEPIYRNGQYVGKTTS\SAY SYSLERHVCLG\FVHNFSEDTGEEQ VVTADFINRG
3945	9442	A	4228	1	1236	
3946	9443	B	4229	1	1742	MKRDNSGGCLPAPASAWPARPRQQ AEWRALTRGPANHCGIISTLGEPPE TPLIGLRTFQCCRLVTDGRVLAGTV SSEPTDGFRSPAPGPGRRTSAMVLL KLGKTPGEFFPFLGSSSQPPSHELNI GKRLDDTKILPGNMKDNFWEMGD TGPCGPCSEIHYDRIGGRDAAHLVN QDDPNVLEIWNLVFIQYNRFGNCVE LQASAAFNWNNQRCKTRNRYICQF ADLRRNLNIINDDITGRVHKDRKLL TGDSPFAANALGKLAAQEMMAAY AVSLPKLTALLRVFSTVVRSIGERFS PIRVLRLLRHTTPNYIYQRLIPYVCV LPTTELSINLNMLTENDIPLFRALFL NNITDADARVLLQKRPREGWLTTD AFLYWAQQDFSGVKPLVAQHWEW MTFSADSVSSVHTLTDDLPLESLAD QPGAGNVHLLIPPEGLLYRSLTLPN AKYKLTAQTLQWLAEETLPDNTQD WHWTVVDKQNESVEDCLIPLFGKP QGKGCLEKSVWAAGRPFSYAGDK NRQLTRYSDTRWHEDSVRNRWFSV MVGPSVRVNEWFSAYAMAGMAYS RVSTFSGDYLRVTDNKGS*
3947	9444	A	4230	1	638	
3948	9445	A	4231	1377	1746	
3949	9446	B	4232	1	1716	MSQYYQPQRPPEHIELDSHAKFFPH HHLQVADSAAHLAASPLRRTHRAL TWAQALPQEEGSGAPSPPGAPSPTP KSFGRTMSASAVFILDVKGKMESC YVVQDVLNSWSPAIPLLQPPKVSDD SGGHHIEECQCLPVYSFLYKTIEVGI LRILQGAGGGEHPDNFVIVYELLDE LMDFASRRPPTARSCRIHHSAEQQA GDGQVTGAPTVTNAVSWRSEGIKS MQRQRPSERNRRYHQAQVFLSGMP ELRLGLNDRVSSSSLAAKGQFKKSQ WPTVWRYLCLYPAMRLPQIQDQCG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRQVCAGRNVVIWSIKSFPGGKEYL MRAHFGLPRWKRKRWRAGPPSGSS LDPLLHRLWDPGPIMKIIEKSGYQA LPWVRTSPRVAIPTSYQLEGRRDGG LNTGFLTAPDADFRGRAGEEPAGR AGVSGWGAGTESSAAGCTAAAPRE GCSASARRLLRADSAGLGRAGGFA GRQCRHAAGGGCAGDRLSGAAAR GDVQECAAFCTGSWCIPTPSTLRQD GAAGFIVPPQSPFEGHDVWQHRHR PELLKQGASPNVQDTSGTVQSMTQ PALDSWTP*
3950	9447	A	4233	1	372	
3951	9448	B	4234	48	1158	MSASAVFILDVKGKPLISRNYKGDV AMSKIEHFMPLLVQREEEGALAPLL SHGQVHFLWIKHSNLYLVATTSKN ANASLVYSFLYKTIEVFCEYFKELE EESIRDNVVIVYELLDELMDFGFPQ TTDSKILQEYITQQSNKLETGKSRVP PTVTNAVSWRSEGIKYKKNEVFIDV IESVNLLVNANGSVLLSEIVGTIKLK VFLSGMPELRLGLNDRVLFELTGRS KNKSVELEDVKFHQCVRLSRFDND RTISFIPPDGDFELMSYRLSTHVKPLI WIESVIEKFSHSRVEIMVKAKGQFK KQSVANGVEISVPVPSDADSPRFKT SVGQRQVCAGEKRRYFGVLSLSGG AREYLMRAHFGLPKCEKERX*
3952	9449	B	4235	153	458	KKDLSLEEIQKKLEAAEERRKSHEA EVLKQLAEKREHEKEVLQKAIEEN NNFSKMAEEKLTHKMEANKENRE AQMAAKLERLREKDKHIEEVRKTK NPRPC*
3953	9450	A	4236	3	182	
3954	9451	A	4237	49	607	NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFE\LILS PRAKEFVPEFPLSPPKEEGFFPGGKF REN*EAA\EERRQSP*SCSS*RQLAE KLRAPRKKCFQKAIEENNNFQ*NGQ KRKLTPHKMEA\NKETPERPQMA\A KLEPFAEEKDKAH*KKCGKNKES\K DP\ADETEAGLI
3955	9452	A	4238	1	356	TELQQEQLQTVVGTYHGSPDQSHQ VTGNHQQPPQQNTGFPR/SNQPYYN SRGVSRGGSRGARGLMNGYRGPAN GFRGGYDGYRPSFSNTPNSGYTQSQ FSAPRDYSGYQRDGYQQNFIP
3956	9453	A	4239	1	2206	RLPPAFSSLSLRSEDALGHQPQRERS KSSGPPPPSGSSGSEAAAGAGAAAP ASQHPATGTGAVQTEAMKQILGVI DKKLRNLEKKKGKLDDYQERMNK GERLNQDQLDAVSKYQEVTNNLEF AKELQRSFMALSQDIQKTIKKTARR EQLMREEAEQKRLKTVLELQYVLD KLGDDEVRTDLKQGLNGVPILSEEE LSLLDEFYKLVDPERDMSLRLNEQY EHASIHLWDLLEGKEKPVCGTTYK VLKEIVERVFQSNYFDSTHNHQNGL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						CEEEEADSAPAVEDQVPEAEPEPAE EYTEQSEVESTEYVNRQFMAETQFT SGEKEQVDEWTVETVEVVNSLQQQ PQAASPSVPEPHSLTPVAQADPLVR RQRVQDLMAQMQGPDNFIQDSML DFENQTLDPAIVSAQPMNPTQNMD MPQLVCPPVHSESRLAQPNQVPVQP EATQVPLVSSTSEGYTASQPLYQPS HATEQRPQKEPIDQIQATISLNTDQT TASSSLPAASQPQVFQAGTSKPLHS SGINVNAAPFQSMQTVFNMNAPVP PVNEPE\TLKQ\QNQSQA\SYNQSFSS \QPSPS*QQTELQQ\EQLQTVVG\TY HGS\QDQSHQ\VTGNHQQ\PPQ\QNT GIST*AIRPYYNSRGVSRGGSRGAR GLMNGYRGP\ANGF́R\GGYDGLPAP SFLLKLPNSGY/SHSPQFQCLPRDYL WPIQRDG/YIQQNFKRGSGQSGPRG APRGRG\GPPRPNRGMPQMNTQQV K
3957	9454	A	4240	1	151	
3958	9455	A	4241	5	120	
3959	9456	A	4242	1	315	EQMVSEDVPC/D/HRVHARIIGSR/G KAIRKIMDEFKVDIRFPQSGAPDPN CVTVTGLPENVEEAIDHILNLEEEYL ADVVDSEALQVYMKPPAHEEAWP CPLRTCSTV
3960	9457	A	4243	107	4057	PFCCGFPGLCVGVRSTMSSVAVLTQ ESFAEHRSGLVPQQIKVATLNSEEES DPPTYKDAFPPLPEKAACLESAQEP AGAWGNKIRPIKASVITQVFHVPLE ERKYKDMNQFGEGEQAKICLEIMQ RTGAHLELSLAKDQGLSIMVSGKL DAVMKARKDIVARLQTQASATVAI PKEHHRFVIGKNGEKLQDLELKTAT KIQIPRPDDPSNQIKITGTKEGIEKAR HEVLLISAEQDKRAVERLEVEKAFH PFIAGPYNRLVGEIMQETGTRINIPPP SVNRTEIVFTGEKEQLAQAVARIKK IYEEKKKKTTTIAVEVKKSQHKYVI GPKGNSLQEILERTGVSVEIPPSDSIS ETVILRGEPEKLGQALTEVYAKANS FTVSSVAAPSWLHRFIIGKKGQNLA KITQQMPKVHIEFTEGEDKITLEGPT EDVNVAQEQIEGMVKDLINRMDYV EINIDHKFHRHLIGKSGANINRIKDQ YKVSVRIPPDSEKSNLIRIEGDPQGV QQAKRELLELASRMENERTKDLIIE QRFHRTIIGQKGERIREIRDKFPEVII NFPDPAQKSDIVQLRGPKNEVEKCT KYMQKMVADLVENSYSISVPIFKQF HKNIIGKGGANIKKIREESNTKIDLP AENSNSETIIITGKRANCEAARSRILS IQKDLANIAEVEVSIPAKLHNSLIGT KGRLIRSIMEECGGVHIHFPVEGSGS DTVVIRGPSSDVEKAKKQLLHLAEE KQTKSFTVDIRAKPEYHKFLIGKGG GKIRKVRDSTGARVIFPAAEDKDQD

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LITIIGKEDAVREAQKELEALIQNLD NVVEDSMLVDPKHHRHFVIRRGQV LREIAEEYGGVMVSFPRSGTQSDKV TLKGAKDCVEAAKKRIQEIIEDLEA QVTLECAIPQKFHRSVMGPKGSRIQ QITRDFSVQIKFPDREENAVHSTEPV VQENGDEAGEGREAKDCDPGSPRR CDIIIISGRKEKCEAAKEALEALVPV TIEVEVPFDLHRYVIGQKGSGIRKM MDEFEVNIHVPAPELQSDIIAITGLA ANLDRAKAGLLERVKELQAEQEDR ALRSFKLSV\TVDPKLHSPGLSGRK GASNSQI\RGLKHDVNIQFP\DKD\D ANQHQD\QITFTGYEKNHSSLPGDAI LRIVG\ELE\QMVSE\DVP\LNHRVSR PASFGARGKSHPPKIMYEF\KV\DIRF PNKSGAPKTPNCVNC*RGFP\ENVE ESHSTQHPSILEEE\YL\ADVV\DSEA LQ\VYMEPP/AHTEEAKGNFSRG\FD VRDAPL\TA\SSSEKAS\DMSSSEEF\P SFWG*RWLPKTLP\WGPKTIMIKKE QNPLPAC
3961	9458	A	4244	11	323	
3962	9459	A	4245	3	171	
3963	9460	B	4246	148	405	XKLSVERKDPLAALAREYGGSKRN ALLKWCQKKTQGYAKRNLLLAFE AAESVGIKPSLELSEMLYTDRPDWQ SVMQYVAQIYKYFET*
3964	9461	A	4247	2	438	AVGGNGGCPRPSRVTSQSTCRFGPR TASHSASRAGLCTASR*VPGWV*CL HFQPLQMPTRDSSFSPDYSAPGRGC GQAGRCGAEHRRPGHRSSCC*NW* CQCSHNLVSSSGTISVEHCAWNHRI PGPRLPEGLFFPH*VCFVVSM
3965	9462	A	4248	3	256	
3966	9463	A	4249	3	444	
3967	9464	A	4250	3	828	VKGVPGVKAERF\E*RMTAKHCALS LVGEPIMYPEINRFLKLLHQCKISSF LVTNAQFPAEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRFLDS VKALAVKQQRTVYRLTLVKAW\NV \ESLQAYAQLGSLGNPDFIEVKGVT YCRESSASSLTMAHVPWHEEVVQF VRELVDLIPEYEIACEHEHSNCLLIA HRKFKIGGEWWTWIDYNRFQELIQ EYEDSGGSKTFSAKDYMARTPHWA LFGASERGFDPKDTRHQRKNKSKAI SGC
3968	9465	A	4251	1	384	
3969	9466	A	4252	3	1225	
3970	9467	A	4253	1	864	
3971	9468	A	4254	1	1266	GNSPPSELKWKAKSEDLRHRGLKA QAEIKGSTQQIGFTTDPRMARSSPYP TDVARVVNAPIFHVNSDDPEAVMY VCKVAAEWRSTFHKDVVVDLVCY RRNGHNEMDEPMFTQPLMYKQIRK QKPVLQKYAELLVSQGVVNQPEYE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						CVSMHGVRNKPSYNSTKSSMDGLI LHPATGLVFVLSKQCEEIHQPVVWT CEQREAENATAEENRVLLAMVNPT VFFDIAVDG\EPLGRVSFEVGRAAA CGNGAQKVGRGRENFRCSEPLERK GFGL*GVPCFHRLFPRVLCVQGGEL QQRH\NGNWWASPILWGRKFERLK NFHP*KPYGSPGILSPWQNAGPQTQ MVPQFF\ICTAQDCSGWNGQAMWV FGTSERKAMNIVEAHWSRFG\SR\N GKTQQRRSPFADCGQLLISLTCVFIF NHPDHSLL
3972	9469	A	4255	3	275	
3973	9470	A	4256	125	315	
3974	9471	A	4257	3	292	
3975	9472	A	4259	1	3045	MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAIINSLPTKKKSRTRWIHSRI LPEVQGGAEKEGILPNSFYEASIILIP KPASDTTKKENFRPISLMNINAKILN KILAKQIRQHIKKLIHHDQVGFIPGM HGLFNICKSVNIIQHINRTNDKNHMI ISIDAEKPFDKIQQHFMLKTLNKLA QNLLKLIGNFSKVSGYKINVQKSQA FLYTNNRQTESQIMNEFPFTIASKRI KYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W/NQKRAHIAKSIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESSEIMPHIYNHLIFDKPD KKKKWGKDSLFNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLKSF CTAKETTIRVNRQPTEWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYAAKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IIKKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKSVWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVIILLHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPCSSAC RRPIVGLQLVMINSGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLTAPL GSTPQAAVCRGPRGRELRAAPADS HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEGCPSLVRASTAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSAAVHHKLKVLHWRS SLSNNKGTGRLYEQVA
3976	9473	A	4260	1	2526	
3977	9474	A	4261	1	3111	

MISSING AT THE TIME OF PUBLICATION

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VDTIAADESFSQVDFGGRLMKDYG ACMSLLSVRVFFKKCPSIVQNFAVF PETMTGAESTSLVIARGTCIPNAEEV DVPIKLYCNGDGEWMVPIGRCTCK PGYEPENSVACKGPVNNTEKAKSG EMWFSPEEYGWEYAAFLALRKCSQ CPEDAVAASGAVALENLMEHGHIR LDKASKDSESSTPHDPTLLFHSGPQP NFRHFQGWNTVTSEGSLIHLPKSKT QSQCPGLFGGSLDSRIDIGGAWYFC HTHTASSASTPSEEAGSLADPSNETE SLLFACTALCSPWECQLILDLASLFQ GIMLMPRAVQFFKCWDKVTVRNQ WRMHSHGPSCLGVSFQKGLCQEM VYISTRGSSSGLRPLVLSLHGWAVD TAIHTCIPFPTDIIWIQDLIAGLKDEW FDTHPGRRIGRPAQLCSSRSGVH
3980	9477	A	4264	1	2653	MGDFNTPLSTLDRSMRQKVNKDIQ ELNSALHQADLIDIYRNLHPESTEYT FFSAPHHTYSKIDHILGSKAPLSKYR RSEIKINCLSDHSAIKLELRIKKLTQ NRSTTWKLNNLLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLWDTL KAVCRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQEIS KIRGELKEIETQKTLQKINESRGWFF EKINKIDRLLARLIKKKREKNQIHAI KNDKGDMSTNHTEIQTTIREYYKHL YANKLENLKEIDKFLETYSLPRLNQ EEVESLNRPITGSEIEAIINSLPNKRS PGPDGFTAKFYQRYKEELLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPTRD MKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNWKKT TLKFIWNQKRARIAKSILSQKNKAG GIMLPDFKLYYKATITKTAWYWYQ NRDIDQWNRTEPSEIMPHIYNHLIFD KPDKNKKWGKDSLFNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRPKTIKTLEENPGNTIQDIGMG EDFMSKTPEAMATKAKIDKWDLIK LKSFCTAKETTIRLNRPPTEWEKIFA IYSSDKGLISRIYNELQQIYEKKTNN PIKKWAKDMNRHLSKEDIYAAKRH MKKCASSLAIREIQIKTTMRYHLTP VRMAIIKKSGNNRCWRGCGEIGTLL HCWWDCKLVQPLWKSVWRFLRDL ELEIPFDPAIPLLGIYPKDYKSCCYE DTCTHMFIVALFTIAKTWNQPKCPT MIDWIKKMWHIYTMEYYADIKKDE FMSFVRTRMKLETIILSKISQ\EKKT KHRMFSLIGGN
3981	9478	A	4265	1	2988	
3982	9479	A	4266	1	2515	MGDFNTPLSTLDRSTRQKVNKDTQ ELNSAPHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHILGSKALLSEC KRTEIITNYLSDDSAIKLELRIKNLT

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QNRSTTWKLNNLLLDDYWVHNEM KAEIKMFFETNENKDTTYQNLWDA FKAVCRGKFVALNAHKRKQGRSKI DTLTSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTVQKINESRSW FFERINKIDRQLARLIKKKREKNLID AIKNDKGDITTDPTEIQTTIREYYKH LYANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPITGSEIVAIINSLTTK KSPGPDGFTAEFYQRAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQKLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLLKEI KEDTNKWKNIPCSWVGRINIVKMAI LPKVIYRFNAIPIKLPMTFFTELKKT TLNFIWNQK\RAHIAKS/VLSQKNKA GGITLPDFKLYYKATVTKTAWYWY QNRDTDQWNRTEPSEIMPRIYNYLI FDKPEKNKQWGKDSLFNKWCWKN WLAICRKLKLDPFLTPYTKINSRWI KDLNIRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKAKIDKWDLI KLKSFCTAKETTNRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMRYH LTLVRMAIIKKSGNNRCWRGRGEIG TLLHCWWDCKLVQSLWKSVWQFL RDLELEIPFDPAIPLL
3983	9480	B	4267	1	2634	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQGDLIDIYRTLHPKSTEYI FFSAPHHTYSKIDHILGSKALLSKCK RTEIITNDLSDHSAIKLELRIKNLTQ NCATTQKLNNLLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLWDAF KAVCRGKFIALHAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQIDAI KNDKGDITTDPTEIRTTVREYYKHL YANKLENLEEMDTFLDTYTLPRLN QEEVESLNRPITGAEIVAIINSLPTKK SPGPDGFTAEFYQRFRKGLRQNSTT FMPKTLNKLGIDGTYLKIIRAIYDKP TANIILNGQKLEAFPLKTGTRQGWP LSPLLFNIVLEVLARAIRQEKEIKGIQ LGKEEVKLSLFADDMIVYLENPIVS AQNLLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKR IKYLGIQLTRDVKDLFKENYKPLLK KIKEDTNKWKNIPCSWVGRINIVKM AILPKVIYRFHAIPIKLPMTFFTELEK TTLKFIWNQKRACIAKSILNQKNKA GGITLPDFKLYYKAIVTKTAWYWY QNRDIDQWIRTEPSEITLHIYKYLIF DKPEKNKQWGKDSLFNKWYWEN WLAICRKLKLDPFLTPYTKINSRWI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KDLNIRPKTIKTLEENLGFTIQDIGM GKNFMSKTPKAMATEAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPLKKWAKDMNRHFSKEDIYAA KKKHMKKCSPSLAIREMQIKTTMRY HLTPVRMTIIKSQETTGAGEDVEK*
3984	9481	A	4268	1	2429	
3985	9482	A	4269	1	2745	
3986	9483	A	4270	1	3210	MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIIMGDFHTP LSTLDRSTRQKVNKDIQELNSALHQ EDLIDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEIITNC LSDHSAIKLELRIKNLTQNRSTTWK LNNLLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTFKAVCRGKF IALNAHKRKQERSKIDTLTSQLKEL EKQEQTHSKASRRQEITKIRAELKEI ETQKTLQNINESRSWFFERINKIDRP LARLIKKKREKNQIDAIKNDKGDIT TDPTEIQTTIREYYKHLYANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAIINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKPFQSIEKEGI LPNSFYEASIILIPKPGRDTTKKENFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVGFIPGMQGWFNIRKSINVI QHINRAKDKNHMIISIDAEKAFDKI QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSGYKINIQKSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFK\ENHKPLLN EIKEDTNKWKNIPCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSERTPHIYNYL IFDKREKNKQWGKDSLFNKWCWE NWLAICRKLKLDPFLTPYTKINSRW IKDLNVRPKTIKTLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGCGEIG TLLHCWWDCKLVQPLWKAVWRFL RDLELEIPFDPAIPLLGIYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF
3987	9484	A	4271	3	3655	
3988	9485	A	4272	1	3615	
3989	9486	A	4273	1	4038	
3990	9487	A	4274	1	3317	MGDFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLQPKSTEYT FFSAPHHTYSKIDHIVGSKALLSKCK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RTEIITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNLLLNDYWVHNEMKA EIKMFFETNENKDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQEITKI RAELKEIETQKTLQKINESRSWFFER INKIDRPLARLIKKKREKNQIDTIKN DKGDITTDPTEIQTTIREYYKHLYA NKLENLDEMDKFLHTYTLPRLNQE EVESLNGPITGAEIVAIIDSLPTKKSP GPDGFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKLGRDT TKKENFRPLSLMNIDAKILNKILAK RIQQHIKKLIHHDQVGFIPGMQGWF NIRKSINVIQHINRGKDKNHMIISID AEKAFDKIQQPFMLKTLNKLGIDGT YFKIIRAIYDKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKAQNLLKLISNFRKVSVY KINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPCSWI GRINIVKMAILPKVIYRFNAIPIKLPT TFFTELEKTILKFIWNQKRAHIAKTI LSQKNKAGGIMLPDFKLYYKATVT KTAWYWYQKRDIDQWNRIELSEIIP HIYNHLIFDKPDKNKKWGKDSVFN KRCWENWLAICRKLKLDTFLTPYT KINSRWIKDLHVRPKAIKTLEENLGI TIQDIGMGKDFTSKTPKAMATKAKI DKWDLIKLKSFCTAKETTIRVNRQP TKWEKIFAIYSSDKGLISRIYKELKQ IYKKKTNNPIKKWAKDMNRHFSKE DIYAANRHMKKCSSSLAIREMQIKT TMRYHLTPVRKAIIKKSGNNRCWR GCGEIGTLLHCWWDCKLVQP\LWK TVWQFLRDLELEIPFYPAIPLLGIYP KDYKSCCYKDTCTRMFIAALFTIAK TWNQPKCPTMIDWIKKMWHIYTM EYYAAIKNDEFMSFVGTWMKLEIII LSKLSQEQKTKHGIFSLIGGN
3991	9488	A	4275	959	2955	
3992	9489	A	4276	1	2870	MKAEIKMFFDTSENKDTTYWNLW DAFKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKASRR QEITKIRAELKEIETQKTLQKINESRS WFFERINKIDRPLARLIKKKREKNQI DAIKNDKGDITTDPTEIQTTIREYYK HLYANKLENLEEMDKFLDTYTLPR LNQEEVESLNRPITGSEIVAIINSLPT KKSPGPDGFTAEFYQSWAETQPKK ENFRPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFNIRK SINVTQHINRAKDKNHMIISIDAEKA FDKIQQPFMLKTLNKLGIDGTYFKII RAIYDNPTANIILNGQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADNMIVY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LENPIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMSQLP FTIASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSG\EG RINIVKMAILPKNWKKTTLKFIWNQ KRARIAKSILSQKNKAGGITLPDFKL YYKATATKTAWYWYQNRDLDQW NRTEPSEITPHIYNYLIFDKPDKNKQ WGKDSLFNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNIRPKTI KTLEENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKQESFCTAK ETTIRVNRQPTKWEKIFATYSSDKG LISRIYSELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKKCPSS LAIREMQIKTTMRYHLTPVRMAIIK KSGNNRCWRGCGEIGTLLHCWWD CKLVQPLWKSVWRFLRDLELEIPFD PAIPLLGIHPKDYKSCCYNDTCTRM FIAALFTIAKTWNQPKCPTIIDWIKK MWHIYTMEYYAAIKNDEFVSFVGT WMKLEIIILSKLSQEQKTTHRIFSLIG GN
3993	9490	A	4277	1	2982	
3994	9491	A	4278	1614	4577	TEPKTKTT*LSQ*MQKKPLTKFSNPS C*KLSIN/IVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENYKQL LKEIKEDTSKWKNIPCSWVGRINIV KMAILPKVIYRFNAIPIKLPMPFFTE LEKTTLKFIWNQKRACIAKSILSQK NKAGGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNKQWGKDSLFNKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKTLEENLGIIIQDI GMGKDFMSKTPKAMATKAKIDKW DLIKLKSFCTAKETTIRVNRQPRKW EKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSPSLAIREMQIKTTM RYHLTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWWDCKLVQPLWNSV WRFLRDLELEIPFDPAIPLLGIYPND YKSCCYKDTCTRMTITSVEEKSQSE KLSYIFLKEKICLMYVGLLNILVSLS GKVPFWLYLGSRLATPPTSSQLFFIG GKERSPDEQGVDILIVLIFRYPSTDS AEQIKKKIEKALYQSLKTKQLSLTIN KPSFRLTRCGIRMTSSNMPLPASSST QRIVQGRETAMEGEWPWQASLQLI GSGHQCGASLISNTWLLTAAHCFW KNKDPTQWIATFGATITPPAVKRNV RKIILHENYHRETNENDIALVQLSTG VEFSNIVQRVCLPDSSIKLPPKTSVF VTGFGSIVDDGPIQNTLRQARVETIS

MISSING AT THE TIME OF PUBLICATION

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPCLMIPSQMLLENFSAAIPGHRCW THMLDNGSAVSTNMTPKALLTISIP PGPNQGPHQCRRFRQPQWQLLDPN ATATSWSEADTEPCVDGWVYDRSV FTSTIVAKWDLVCSSQGLKPLSQSIF MSGILVGSFIWGLLSYRFGRKPMLS WCCLQLAVAGTSTIFAPTFVIYCGL RFVAAFGMAGIFLSSLTLMVEWTTT SRRAVTMTVVGCAFSAGQAALGGL AFALRDWRTLQLAASVPFFAISLIS WWLPESARWLIIKGKPDQALQELR KVARINGHKEAKNLTIETPPPPPPIPI PSPTAPPLSTPTITFTAITPSPPAPPIPS LTPQPPSLQNISTTFTTIVTIGNSTIIN STHTVTSITHHLHLHVARTHLMGVL DVSGETECVYLKVLMSSVKEEVAS AKEPRSVLDLFCVPVLRWRSCAML VVKYAVLGRDLTSSLARSFSLLISY YGLVFDLQSLGRDIFLLQALFGAVD FLGRATTALLLSFLGRRTIQAGSQA MAGLAILANMLVPQDLQTLRVVFA VLGKGCFGISLTCLTIYKAELFPTPV RMTADGILHTVGRLGAMMGPLILM SRQALPLLPPLLYGVISIASSLVVLFF LPET\QGLPLPDTIQDLESQKSTAAQ GNRQEAVTVESTSL
4009	9506	A	4293	3672	3967	LQPPPHGRRGLLHHLSPGHGPHHPP VTPQTRSPAQP/PGQMGPRAPLGCC LPPPPRPPTCRREK*TTETRFSPCWR TRPWGPGPPRPLSRGGPLPCAPA
4010	9507	A	4294	1773	2213	AHWLHLPRLPHHRAQWAAALQPG PAGWGWSWQPQLCSAGRLLCHGAI GRP/LSIFCWTWDLGASSCGHPAAR SMMASGVTWTSRGMGEKRVSSTPF PIFFPAASPPPPSRLPNCPFCHRTLAE RAQHLASVRPGLHLSSPTCCMKCSC
4011	9508	A	4295	1	616	
4012	9509	A	4296	93	502	EERKRPHLGAWWENRKCFFSFQPD FKAAECRETVARPSLSIPQDCLSVSL ADTNQLCLEVRLARGVCRRRAHLS PPVCIQSPLSQGH*LLCSK*SASIIGA GLANFQGTDSLVAEHPVSWIIHNSN FVFHPGYFRL
4013	9510	A	4297	1537	2360	TCCTNVVWGAPPHRDSRVSDRVHS QKSRRACYGQRNKRPGG*G*ILISA KKQLLSPRR*LKVWPMRSASLQSM PLASPSPVCPPGLLFLWP*QALL\PS DCG/PLSLTRLSR*GG\PPRPHWCSR FRWLCARVLL
4014	9511	A	4298	1	493	MEAPAELLAALPALATALALLLAW LLVRRGAAASPEPARAPPEPAPPAE ATGAPAPSRPCAPEPAASPAGPEEP GEPAGLGELGEPAGPGEPEGPGDPA AAPAEAEE/PGGGGEAGTHRGPRGP LPTPGAPAAAAVPRRARERGRGLQ PRLPPGSAEPAARRKCR
4015	9512	A	4299	2	418	
4016	9513	A	4300	8808	9100	RKVLFFFFFEMKSRSVA\RLGCSGTI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SAHCNLCLPGSSDSPASASRVAGMT GAHNHIQLIFVFLVGMGFHHVGQA GLELLT*VIHPPQSPKVLGLQV
4017	9514	A	4301	3	101	
4018	9515	C	4302	5673	5894	MWQLTPAILALGEIEAGGLFEPRRV KLAWPAQEELVSTKNTKISWVWW RAPVVPATQEAEVGGSLELERSRLQ *
4019	9516	A	4303	1	241	
4020	9517	A	4304	58	180	
4021	9518	A	4305	2	325	FFFFFFFFFFFETESLSVTQAGEPGHD LGSLEPPPPRFKQFSCLSLPSS\WIYR HVPPCPANFFFFLVETGFHHVGQAG LKLLTSNDPPASASQSSGIRGVSHLT RLVS
4022	9519	A	4306	206	386	
4023	9520	A	4307	2	260	
4024	9521	A	4308	5	227	
4025	9522	A	4309	676	1076	FLLCFPPCLSPKFFLFLLGKIYSQSN WCVIVNWRIELGWMFNKICDSKIIF SLGSFLCKIKAHWGLWKSPTTSFQE RSPFFSSLFRAMRAKPSRSMD/RLFF ELLVKSLPVASPVEPLSVIAEQSSQI CPCHGI
4026	9523	A	4310	3	205	
4027	9524	A	4311	3	345	
4028	9525	A	4312	118	7473	
4029	9526	A	4313	1	297	
4030	9527	A	4314	366	504	
4031	9528	A	4315	1	2899	MDAPKAGYAFEYLIETLNDSSHKKF FDVSKLGTKYDVLPYSIRVLLEAAV RNCDGFLMKKEDVMNILDWKTKQ SNVEVPFFPARVLLQDFTGIPAMVD FAAMREAVKTLGGDPEKVHPACPT DLTVDHSLQIDFSKCAIQNAPNPGG GDLQKAGKLSPLKVQPKKLPCRGQ TTCRGSCDSGELGRNSGTFSSQIENT PILCPFHLQPVPEPETVLKNQEVEFG RNRERLQFFKWSSRVLKNVAVIPPG TGMAHQINLEYLSRVVFEEKDLLFP DSVVGTDSHITMVNGLGILGWGVG GIETEAVMLGLPVSLTLPEVVGCEL TGSSNPFVTSIDVVLGITKHLRQVG VAGKFVEFFGSGVSQLSIVDRTTIA NMCPEYGAILSFFPVDNVTLKHLEH TGFSKAKLESMETYLKAVKLFRND QNSSGEPEYSQVIQINLNSIVPSVSG PKRPQDRVAVTDMKSDFQACLNEK VGFKGFQIAAEKQKDIVSIHYEGSE YKLSHGSVVIAAVISCTNNCNPSVM LAAGLLAKKAVEAGLRVKPYIRTSL SPGSGMVTHYLSSSGVLPYLSKLGF EIVGYGCSTCVGNTAPLSDAVLNA VKQGDLVTCGNFIWK\KNFEGRLC DCVRANYLASPPLVVAYAIAGTVNI DFQTEPLGTDPTGKNIYLHDIWPSR EEVHRVEEEHVILSMFKALKDKIEM

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNKRWNSLEAPDSVLFPWDLKSTY IRCPSFFDKLTKEPIALQAIENAHVL LYLGDSVTTDHISPAGSIARNSAAA KYLTNRGLTPREFNSYGARRGNDA VMTRGTFANIKLFNKFIGKPAPKTIH FPSGQTLDVFEAAELYQKEGIPLIIL AGKKYGSGNSRDW\AAKGPYLLGV KAVLAESYEKIHKDHLIGIGIAPLQF LPGENADSLG\LSGRETFSLTFPEELS PG\ITLNIQTSTGKVFSVIASFEDDV\ EITL\YKHG\GLLNFV\ARKFS
4032	9529	A	4316	1	178	
4033	9530	A	4317	165	403	PSSRSRAPSPTPTLCGASCCPTCPAC FPAPSRRAGAAGGAG*RPRGGPTST TCYGPTETWLYQLQTVGSRNTTRT PKST
4034	9531	A	4318	3	404	
4035	9532	A	4319	3	217	
4036	9533	A	4320	3	423	SFFIHRTKGKGPLMSSSFKKLYFSLT TEALSFAKTPS/CQGQGCDKTRSRV TLQEWNDPLDHDLEAQLIYRHLLG VEAMLWERHRELSGGAEAGTMPTS PGKVPEDSLARLLRVLQDLREAHSS SPAGSPPSEPNCLLELQ
4037	9534	A	4321	2	3040	DPGVWLPPSRDPAMAKRSSLYIRIV EGKNLPAKDITGSSDPYCIVKVDNE PIIRTATVWKTLCPFWGEEYQVHLP PTFHAVAFYVMDEDALSRDDVIGK VCLTRDTIASHPKGFSGWAHLTEVD PDEEVQGEIHLRLEVWPGARACRL RCSVLEARDLAPKDRNGTSDPFVR VRYKGRTRETSIVKKSCYPRWNETF EFELQEGAMEALCVEAWDWDLVS RNDFLGKVVIDVQRLRVVQQEEGW FRLQPDQSKSRRHDEGNLGSLQLEV RLRDETVLPSSYYQPLVHLLCHEVK LGMQGPGQLIPLIEETTSTECRQDV ATNLLKLFLGQGLAKDFLDLLFQLE LSRTSETNTLFRSNSLASKSMESFLK VAGMQYLHGVLGPIINKVFEEKKY VELDPSKVEVKDVGCSGLHRPQTE AEVLEQSAQTLRAHLGALLSALSRS VRACPAVVRATFRQLFRRVRERFPG AQHENVPFIAVTSFLCLRFFSPAIMS PKLFHLRERHADARTSRTLLLLAKA VQNVGNMDTPASRAKEAWMEPLQ PTVRQGVAQLKDFITKLVDIEEKDE LDLQRTLSL*APPVKEGPLFIHRTKG KGPLMSSSFKKLYFSLTTEALSFAK MPSSKKSALIKLANIRAAEKVEEKS FGGSHVMQVIYTDDAGRPQTAYLQ C/KGVPFCVRVQSHWEK**YQGHQI YLAGSGIPTSVAKGPAAAEIQPTPAS WAPTIPVPSVGTSGAAATKKTRQC VNELNQWLSALRKVSINNTGLLGS YHPGVFRGDKWSCCHQKEKTDTDF RSVPQTGVQWRDLGSLQSPPPRVK QFSCLNLPSSWDDRHSPPSLANFFV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						F*LEMGFHHVSQAALVLLLLLLLLL FDTESRSIIQAGVQWCNLGSLQSPFP RLG*FSCLSLPSTTGASHCTQLSQGC DKTRSRVTLQEWNDPLDHDLEAQL IYRHLLGVEAMLWERHRELSGGTE AGTVPTSPGKVPEDSLARLLRVLQD LREAHSSSPAGSPPSEPNCLLELQT
4038	9535	A	4322	308	658	
4039	9536	A	4323	1	2662	MAKRSSLYIRIVEGKNLPAKDITGSS DPYCIVKVDNEPIIRYRPHPQDRGA LSLSSARALPAKGTATVWKTLCPF WGEEYQVHLPPTFHAVAFYVMDE DALSRDDVIGKVCLTRDTIASHPKG FSGWAHLTEVDPDEEVQGEIHLRLE VWPGARACRLRCSVLEARDLAPKD RNGTSDPFVRVRYKGRTRETSIVKK SCYPRWNETFEFELQEGAMEALCV EAWDWDLVSRNDFLGKVVIDVQR LRVVQQEEGWFRLQPDQSKSRRHD EGNLGSLQLEVRLRDETVLPSSYYQ PLVHLLCHEVKLGMQGPGQLIPLIE ETTSTECRQDVATNLLKLFLGQGLA KDFLDLLFQLELSRTSETNTLFRSNS LASKSMESFLKFALHVYLAPSWAD TAGKRCKGGCREKVGSWSGTGGD RINVTCGGPQVAGMQYLHGVLGPII NKVFEEKKYVELDPSKVEVKDVGC SGLHRPQTEAEVLEQSAQTLRAHLG ALLSALSRSVRACPAVVRATFRQLF RRVRERFPGAQHENVPFIAVTSFLC LRFFSPAIMSPKLFHLRERHADARTS RTLLLLAKAVQNVGNMDTPASRAK EAWMEPLQPTVRQGVAQLKDFITK LVDIEEKDELDLQRTLSLQAPPVKE GPLFIHRTKGKGPLMSSSFKKLYFSL TTEALSFAKTPSSKKSALIKLANIRA AEKVEEKSFGGSHVMQVIYTDDAG RPQTAYLQCKCVNELNQWLSALRK VSINNTGLLGSYHPGVFRGDKWSC CHQI*I\TGQG\CDKTRVTG*PCREW NDLLDRDLE\SQLIYRHLLGVEAML WERHRELSGGAEAGTVPTKPLAKV PEDSLARLAPGCLQDLREAH\SSSPA GSPPSEPNLASLEAADVRPALRSPC
4040	9537	A	4324	69	194	
4041	9538	A	4325	1350	2203	TWRLDPQIISSPKPQPGGTYTLEVV KSSKSKKVLSPHP*WPPLRLWQR\G GSPEGGTQAPDGSLPPPPPRPKSERV GSPKLSGGKR/EGSHPGPPHITHP/ DGEEKAKSSWFGLREAKDPTQKPS PHPVKPLSAAPVEGSPDRKQSRSSL SIALSSGLEKLKTVTSGSIQPVTQAP QAGQMVDTKRLKDSAVLDQSAKY YHLTHDELISLLLQRERELSQRDEH VQELESYIDRLLVRIMETSPTLLQIPP GPPK
4042	9539	A	4326	2	761	
4043	9540	A	4327	2	410	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4044	9541	A	4328	295	780	
4045	9542	A	4329	1	2203	
4046	9543	A	4330	1	190	RFIMLVRLVFNS*PQ/CDPPASASQS AGITGMSHRARPELSVLTQGFRNW AFRLLLQCHSPDFF
4047	9544	A	4331	2	269	
4048	9545	A	4332	3	223	DFEPSLQHCSSKLCRNILRASSCHSS WGRM*FPGSV*PTWKI*REESCEWS RTAINPKYKILLHGFVVRTVWR
4049	9546	A	4333	2	366	PCSEPPTRRSGATPSPHPGGCGAKL CRNILRASSCHSSWGRM*FPGSV*P TWKI*REESCEWSCTAINPSTRSCCT VCGTNCLEETPTTCPSTRGLQCGRG LTRATGNCPRNDGLTLLSLN
4050	9547	A	4334	3	131	
4051	9548	A	4335	923	1442	GGPCLCRPSWPAVLQVRSGLPTSIPS PWPLFCLPQSILLGPLEMPG*RPLLQ RPFYRMSLRTCQRRVRCWTWSVRC RTAWHTRVFLKLPDTFTNDSSTTGF *AKPSALLLSTGWS*WATA/CGGGA AALLATMLRAAYPAGQVLRLLPSP PAPGAKLCRNILRASSCHSSWGRM
4052	9549	A	4336	1	137	
4053	9550	A	4337	876	1012	
4054	9551	A	4338	148	278	
4055	9552	B	4339	7	673	MVEVTILMIMGLYRIYGFAVAVVS MILSYNVCSEGEVVSVMFSFVVTSS SCGMHRSTLLSSVYSHLIFDSAYVIN NVADALSRGFSMHCMHCDNLKTC HTSHGSVMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHVAKY AEIFGLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPWFIKX *
4056	9553	A	4340	786	1088	
4057	9554	A	4342	1	66	
4058	9555	A	4343	2	80	
4059	9556	A	4344	8	258	
4060	9557	A	4345	5	383	
4061	9558	A	4346	99	634	TTTMSSKRTKTKTTKKRPQRATSN VFAMFDQSQIQEFKEAFNMIDQNR DGFIDKEDLHDMLASLGK\NPTDAY LDAMMNEAPGPINFTMFLTMFGEK LNGTDPEDVIRNAFACFDEEA\TGTI QEDYLRE\LLTTMGDRFTDEE\VDEL YREAPY*QKGGISNYIEFTRILTGRP PKHKDD
4062	9559	A	4347	1	966	
4063	9560	A	4348	3	215	
4064	9561	A	4349	1	1416	NSGGSGGGTSGSGSSSGQGKMGQS QSGGHGPGGGKKDDEDKKKKYEPP VPTRVGKKKKKTKGPDAASKLPLV TPHTQCRLKLLKLERIKDYLLMEEE FIRNQEQMKPLEEKQEEERSKVDDL RGTPMSVGTLEEIIDDNHAIVSTSVG SEHYVSILSFVDKDLLEPGCSVLLN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HKVHAVIGVLMDDTDPLVTVMKV EKAPQETYADIGGLDNQIQEIKESV ELPLTHPEYYEEMGIKPPKGVHPFG PTWPRVKTLLAKAVANQTS\ASFLR \VVGYELIQKYLGDGPKLVRELFRV A\EEHAPSIVFIDEIDAIGT\KRY\DSN SGGE\REFHRTNVGN*LEPVGMGFD SRG\DV\KVFPWATNRI\ETL\DPALI\ RPGRI\DR\KNEFPLPDEKTKKRIFQI HTSRMTLADDVTL\DDLIHGLKIDLS GA\DI\KAIC\TEAGL\MGL*GERRMK VTNEDFKKSKENVLYKKQEGTPEG LYL
4065	9562	A	4350	2	70	
4066	9563	A	4351	1	1605	
4067	9564	A	4352	3	193	
4068	9565	A	4353	3	127	LFHPCQDSQQHH*CVCCRLTGHGA A*VHGPCQAVQTYRASH
4069	9566	A	4354	2	323	
4070	9567	A	4355	3	85	
4071	9568	A	4356	49	413	
4072	9569	A	4357	3	338	
4073	9570	A	4358	1	3735	
4074	9571	A	4359	2	317	
4075	9572	B	4360	2576	2685	MDGKNSSGSKRYNRKRELSYPKNE SFNNQSRRSSSQKSKTFNKMPPQRG GGSSKLFSSSFNGGRRDEVAEAQRA EFSPAQFSGPKKINLNHLLNFTFEPR GQTGHFEGSGHGSWGKRNKWGHK PFNKELFLQANCQFVVSEDQDYTA HFADPDTLVNWDFVEQVRICSHEV PSCPICLYPPTAAKITRCGHIFCWAC ILHYLSLSEKTWSKCPICYSSVHKK DLKSVVATESHQYVVGDTITMQLM KREKGVLVALPKSKWMNVDHPIHL GDEQHSQYSKLLLASKEQVLHRVV LEEKVALEQQLAEEKHTPESCFIEA AIQELKTREEALSGLAGSRREVTGV VAALEQLVLMAPLAKESVFQPRKG VLEYLSAFDEETTEVCSLDTPSRPLA LPLVEEEEAVSEPEPEGLPEACDDLE LADDNLKEGTICTESSQQEPITKSGF TRLSSSPCYYFYQAEDGQHMFLHP VNVRCLVREYGSLERSPEKISATVV EIAGYSMSEDVRQRHRYLSHLPLTC EFSICELALQPPVVSKETLEMFSDDI EKRKRQRQKKAREERRRERRIEIEE NKKQGKCPEVHIPLENLQQFPAFKF LYLLLFEKPRKETGKNVAMKAENR CRRRPPPALNAMSLGPRRARSAPTA VAAEAPVDAAELPQRRRHRLRHGQ EQRLQQLLRLFGQQQRATAAPLRL GGASRRV*
4076	9573	A	4361	3	93	
4077	9574	A	4362	1	289	VGNPQQEVQNIFKAKHPMDTEVTK AKIIGFGSALLEEVDPNPANFVGAGI IHTKTTQIGCLVRLEPNLQAQMYRL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						T/LRTSKEAVSQRLCELLSAQF
4078	9575	A	4363	1	275	
4079	9576	A	4364	2	2803	RGLAVFISDIRNCKSKEAEIKRINKE LANIRSKFKGDKALDGYSKKKYVC KLLFIFLLGHDIDFGHMEAVNLLSS NRYTEKQIGYLFISVLVNSNSELIRLI NNAIKNDLASRNPTFMGLALHCIAS VGSREMAEAFAGEIPKVLVAGDTM DSVKQSAALCLLRLYRTSPDLVPM GDWTSRVVHLLNDQHLGVVTAAT SLITTLAQKNPEEFKTSVSLAVSRLS RIVTSASTDLQDYTYYFVPAPWLSV KLLRLLQCYPPPDPAVRGRLTECLE TILNKAQEPPKSKKVQHSNAKNAV LFEAISLIHHDSEPNLLVRACNQLG QFLQHRETNLRYLALESMCTLASSE FSHEAVKTHIETVINALKTERDVSV RQRAVDLLYAMCDRSNAPQIVAEM LSYLETADYSIREEIVLKVAILAEKY AVDYTWYVDTILNLIRIAGDYVSEE VWYRVIQIVINRDDVQGYAAKTVF EALQAPACHENLVKVGGYILGEFG NLIAGDPRSSPLIQFHLLHSKFHLCS VPTRALLLSTYIKFVNLFPEVKPTIQ DVLRSDSQLRNADVELQQRAVEYL RLSTVASTDILATVLEEMPPFPERES SILAKLKKKKGPSTVTDLEDTKRDR SVDVNGGPEPAPASTSAVSTPSPSA DLLGLGAAPPAPAGPPPSSGGSGLL VDVFSDSASVVAPLAPGSEDNFARF VCKNNGVLFENQLLQIGLKSEFRQN LGRMFIFYGNKTSTQFLNFTPTLICS DDLQPNLNLQTKPVDPTVEGGAQV QQVVNIECVSDFTEAPVLNIQVHGS GGT\FQN\VSLQLPITLNKFFQPT\EK FCQDFFQRWKQTSNPQQEVHNIFK AKHPMDTEFTK\AKIIG\FGSELLAE VDPNPANFVGAG\II\HTKTTQI\GCP LRL*PNLQAQMY\RLTLRTSKEAVS\ Q\RLCELLSAQF
4080	9577	A	4365	2	231	
4081	9578	A	4366	1	224	
4082	9579	A	4373	131	381	
4083	9580	A	4374	93	449	
4084	9581	A	4375	11	594	
4085	9582	A	4376	1	1410	
4086	9583	A	4377	1	66	
4087	9584	A	4378	1	553	RRGPLSQNGSFGPSPVSGGECSPPLT VEPPVRPLSATLNRRDMPRSEFGSV DGPLPHPRWSAEASGKPSPSDPGSG TATMMNS\SS*GSSPTRVLDEGMQT VLQEPEVPSVPSITSLAERPVAVNM APKGPPPFPGVPLMSTPMGGPVPPPI RYGPPPQLCGPFGPRALPPPFGPGM RPPLCLRE
4088	9585	A	4379	1	3589	AFLSKVEEDDYPSEELLEDENAINA KRSKEKNPGNQGRQFDVNLQVPDR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AVLGTIHPDPEIEESKQETSMILDSE KTSETAAKGVNTGGREPNTMVEKE RPLADKKAQRPFERSDFSDSIKIQTP ELGEVFQNKDSDYLKNDNPEEHLK TSGLAGEPEGELSKEDHGNTEKYM GTESQGSAAAEPEDDSFHWTPHTSV EPGHSDKREDLLIISSFFKEQQSLQR FQKYFNVHELEALLQEMSSKLKSA QQESLPYNMEKVLDKVFRASESQIL SIAEKMLDTRVAENRDLGMNENNI FEEAAVLDDIQDLIYFVRYKHSTAE ETATLVMAPPLEEGLGGAMEEMQP LHEDNFSREKTAELNVQVPEEPTHL DQRVIGDTHASEVSQKPNTEKDLDP GPVTTEDTPMDAIDANKQPETAAEE PASVTPLENAILLIYSFMFYLTKSLV ATLPDDVQPGPDFYGLPWKPVFITA FLGIASFAIFLWRTVLVVKDRVYQV TEQQISEKLKTIMKENTELVQKLSN YEQKIKESKKHVQETRKQNMILSDE AIKYKDKIKTLEKNQEILDDTAKNL RVMLESEREQNVKNQDLISENKKSI EKLKDVISMNASEFSEVQIALNEAK LSEEKVKSECHRVQEENARLKKKK EQLQQEIEDWSKLHAELSEQIKSFE KSQKDLEVALTHKDDNINALTNCIT QLNLLECESESEGQNKGGNDSDEL ANGEVGGDRNEKMKNQIKQMMDV SRTQTAISVVEEDLKLLQLKLRASV STKCNLEDQVKKLEDDRNSLQAAK AGLEDECKTLRQKVEILNELYQQKE MALQKKLSQEEYERQEREHRLSAA DEKAVSAAEEVKTYKRRIEEMEDE LQKTERSFKNQIATHEKKAHENWL KARAAERAIAEEKREAANLRHKLL ELTQKMAMLQEEPVIVKPMPGKPN TQNPPRRGPLSQNGSFGPSPVSGGE CSPPLTVEPPVRPLSATLNRRDMPR SEFGSVDGPLPHPRWSAEASGKPSP SDPGSGTATMMNSSSRGSSPT\RVL DEGK\VNMGPK\GAPSFPKEFPL\MS TPMGGPV\PPPIRYGPPPQLCGPFGP RHLPPPFGPGMRPPLGLREFAPGVP PGRRDLPLHPRGFLPGHAPFRPLGS LGPREYFIPGTRLPPPTHGPQEYPPP PAVRDLLPSGSRDEPPPASQSTSQD CSQALKQSP
4089	9586	A	4380	3	148	
4090	9587	A	4381	1885	2826	CLQEAIMDGTEIAVSPRSLHSELMC PICLDMLKNTIGSA*ASVPLTDHSGL PFSYPRNKECPTCRKKLVSKRSLRP DPNFDALISKIYPSREEYEAHQDRV LIRLSRLDRGGTLGGGTLGPPSPPGA PSPPEPGGDPYLQSSSEALWL*ACPP SHSRYVKTTGNATVDHLSKYLALRI ALERRQQQEAGEPGGPGGGASDTG GPDGCGGEGGGAGGGDGPEEPALP SLFHLLQLSSLFSPLSLLPPPQTLNGS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LTLELVNSPRRPLPRQGLTLRALSLP GSPQHPGKLLTGGCALGFSTPATLH TGKQPYVCAT
4091	9588	A	4382	2	456	DRGGTLGGGTLGPPSPPGAPSPPEP GGDPYLQSSSEALWL*ACPPSHSRY VKTTGNATVDHLSKYLALRIALERR QQQEAGEPGGPGGGASDTGGPDGC GGEGGGAGGGDGPEEPALPSLFHLL QLSSLFSPLSLLPPPQTLNGSLTLEL V
4092	9589	A	4383	58	1262	CLQEAIMDGTEIAVSPRSLHSELMC PICLDMLKNTMTTKECLHRFCSDCI VTALRSGNKECPTCRKKLVSKRSLR PDPNFDALISKIYPSREEYEAHQDRV LIRLSRLHNQQALSSSIEEGLRMQA MHRAQRVRRPIPGSDQTTTMSGGE GEPGEGEGDGEDVSSDSAPDSAPGP APKRPRGGGAGGSSVGTGGGGTGG VGGGAGSEDSGDRGGTLGGGTLGP PSPPGAPSPPEPGGEIELVFRPHPLLV EKGEYCQTRYVKTTGNATVDHLSK YLALRIALERRQQQEAGEPGGPGG GAS\NTEELNVCGGEGGGAGGGDG\ PKEPA\LPSLEGVSEKQYTIYIAPGG GAFTTL\NGSLT\LELVNE\KFWKVS RP\LELCYAPHPRIQSDPHPGDKPEE RGPLG
4093	9590	A	4384	3	221	
4094	9591	A	4386	2	271	
4095	9592	A	4387	54	990	HSIMMKIPWGSIPVLMLLLLLGLIDI SQAQLSCTGPPAIPGIPGIPGTPGPDG QPGTPGIKGEKGLPGLAGDHGEFGE KGDPWIPGNPGKVGPKGPMGPKGG PGAPG\APGPKG\DSGDYKATQKIAF SATRTINVP/LLRRSQT\IRFRPRCITN MNT\NYE\PRSGKFTLQGCPGLY*FN LSTPSSRG\NLCVN\LMRGRERAQE/ VWVTFC\DYCLTNTFPGSPQGGNGP QLKKAPKGGGGGEKKTVLPAGPPN KNFTYWGMGGCPTAIFSGFLAFFQI WEGLTCGLASHPTPAPPAQQRSLYP QQQPYDQAKCTQ
4096	9593	A	4388	3	493	
4097	9594	B	4389	272	2158	MGPLMVLFCLLFLYPGLADSAPSCP QNVNISGGTFTLSHGWAPGSLLTYS CPQGLYPSPASRLCKSSGQWQTPGA TRSLSKAVCKPVRCPAPVSFENGIY TPRLGSYPVGGNVSFECEDGFILRG SPVRQCRPNGMWDGETAVCDNGA GHCPNPGISLGAVRTGFRFGHGDKV RYRCSSNLVLTGSSERECQGNGVW SGTEPICRQPYSYDFPEDVAPALGTS FSHMLGATNPTQKTKESLGRKIQIQ RSGHLNLYLLLDCSQSVSENDFLIF KESASLMVDRIFSFEINVSVAIITFAS EPKVLMSVLNDNSRDMTEVISSLEN ANYKDHENGTGTNTYAALNSVYL MMNNQMRLLGMETMAWQEIRHAI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ILLTDGKSNMGGSPKTAVDHIREIL NINQKRNDYLDIYAIGVGKLDVDW RELNELGSKKDGERHAFILQDTKAL HQVFEHMLDVSKLTDTICGVGNMS ANASDQERTPWHVTIKPKSQETCR GALISDQWVLTAAHCFRDGNDHSL WRVNVGDPKSQWGKEFLIEKAAIS PGFDVFAKKNQGILEFYGDDIALLK LAQKVKMSTHARPICLPCTMEANL ALRRPQGSTCRDHENELLNKQSVL CTFWSPLNGSKPKI*
4098	9595	A	4390	2	201	
4099	9596	A	4391	1	130	
4100	9597	A	4392·	2	215	
4101	9598	A	4393	3	300	
4102	9599	A	4394	3	310	
4103	9600	A	4395	2	228	
4104	9601	A	4396	2	448	PRVRKDAVRDGLRAVKNAIDDGCV V/PGAGAVEVAMAEALNKYKLSVK GKAQLGVQAFADALLVIPKVLAQN SGFDLQETLVKI*AEHSESGQLVGV DLNTGEPVVAAEAGI\WDNDCVKK QLLHSCTVIATNILLVDEIMRAGMS SLKG
4105	9602	A	4397	2	100	
4106	9603	A	4398	3	174	
4107	9604	A	4399	1	147	
4108	9605	A	4400	1	104	
4109	9606	A	4401	153	480	TTLKQQFSFMSYKAVKLKVFLIMSC YPRNPSHFP*CGA/WVMCPLRVGSE RRLCPFMATS\QSLSNKFHNRKIFMS REIKFRRNLLKKNETQLMYLQIFRW YTKQRLFLF
4110	9607	A	4402	1	186	
4111	9608	A	4403	3	478	
4112	9609	B	4404	56	390	XAAYVQPFLDKSGLEKYLYPASAA APFPLLYPGIPAAAAAFPCLSSVLSP PPEKAGAAAATLLPHEVAPLGAPHP QHPHGRTHLPFAGPREPGNPESSAQ EDPSQPGKEAP*
4113	9610	A	4405	2	485	
4114	9611	A	4406	105	183	
4115	9612	A	4407	1	1560	MLRKKEKANYRLLAERTRKRPRKA SAELQRKHYLPMLRGHLRLFLPGRL RPLPSNPRLAFPAAERGGGHCGPMR HFPVSTQERGTADPVHPASPLPPNQ APNAGHSPPTPRSPPNTSSPRRRRRR PESGWGRPGGGFTSILRPDSPLPTRV QYGTERKRRGQSSRDAFSARRQSV GGGANWEGGGAKRARRGTGPAG WRAEGGGAACRGSARASPAFRGRG PLPPFASGRVPGRQCGLRQWLQEK LLGPSDHLSCFQMPGTSVCDCAACL RACTEKPCDSNMWDSQAPWTGLK TRLTYRIFTINDLRQDWWRDYFEK YGKIETIEVMEDRQSGKKRGFAFVT FDDHDTVDKIVGRGGGSGNFMGRG

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNFGGGGGNFGRGGNFGGRGGYG GGGGGSRGSYGGGDGGYNGFGGD GGNYGGGPGYSSRGGYGGGGPGY GNQGGGYGG/G/GGGYDGYNEGGN FGGGNYGGGGNYNDF\GNYSG\QQ QS\NYGPMKGGSLGG\RSSGSPYGG GYGSG\G\GSGGYGSRRF
4116	9613	A	4408	2	370	
4117	9614	A	4409	1	159	
4118	9615	A	4410	3	261	
4119	9616	A	4411	1	8748	
4120	9617	A	4412	1	2176	
4121	9618	A	4413	37	441	
4122	9619	A	4414	1	1940	PVLRHAVWLKSEGKSSFGLCAPLR KGSFLQKSWIFFRPVMADKLTRIAI VNHDKCKPKKCRQECKKSCPVVR MGKLCIEVTPQSKIAWISETLCIGCG ICIKKCPFGALSIVNLPSNLEKETTH RYCANAFKLHRLPIPRPGEVLGLVG TNGIGKSAALKILAGKQKPNLGKY DDPPDWQEILTYFRGSELQNYFTKI LEDDLKAIIKPQYVDQIPKA\AKGTV GSILDRKDETKTQAIVCQQLDLTHL KERNVEDLSGGELQRFACAVVCIQ KADIFMFDEPSSYLDVKQRLKAAITI RSLINPDRYIIVVEHDLSVLDYLSDFI CCLYGVPSAYGVVTMPFSVREGINI FLDGYVPTENLRFRDASLVFKVAET ANEEEVKKMCMYKYPGMKKKMG EFELAIVAGEFTDSEIMVMMLGENG MGKTTFIRMLAGRLEPDEEGEVPVL NVSYKLQKISPKSTGSVRQLLREKIR DAYTHPQFVTNVMKPLQIENIIDQE VQTLSGGELQRVT\LAL*LGQNLPD VYLI\DEPPA\YLDS\EQRLMAARVV KRFIPHAKKTA\FVVGTWTFIM\ATY L\ADRVIVFD\GVPSTKNTVANSPQT\ LLAGMNKFLSQLEITFRRDPNNYRP RINKLNSIKDVEQKKSGN\YFFLDD
4123	9620	A	4415	1	122	
4124	9621	A	4416	2	1382	
4125	9622	A	4417	135	282	
4126	9623	A	4418	2	1652	
4127	9624	A	4419	3	279	
4128	9625	A	4420	8	353	
4129	9626	A	4421	1	1542	
4130	9627	A	4422	1	496	
4131	9628	A	4423	70	365	
4132	9629	A	4424	1	3771	
4133	9630	A	4425	2	285	
4134	9631	A	4426	1	724	
4135	9632	A	4427	58	197	
4136	9633	A	4428	640	813	
4137	9634	A	4429	3	268	
4138	9635	A	4430	1	1512	
4139	9636	A	4431	3	1625	
4140	9637	A	4432	1	330	GKTITLEVEPSDTIENVKAKIQDKEG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IPPDQQRLIFAGKQLEDGRTLSDYNI QKESTLHLVLRLRGGI\KYNCDKMI CRKCYARLHPRAVNCRKKKCGHT NNLRPKKKVK
4141	9638	A	4433	2	544	DPRLQFFFFFLSSLLQRGDRAGWW RRFFGTQTCRVFVKTL\TGKNLHPL RYETQ*HPLKNVQKPKISRTKEGIP\ PDQAAS**FAGK\QLE\DGRT\LSDY\ NIQKESTRAPWLLRLR\GGIIEPFSPP GLPKKYN\CDKMI\CRKCYAR/LFHP RCLSTCRK\KKCGSHQTTLRPQRRR SNKGGFFP
4142	9639	A	4434	385	499	
4143	9640	A	4435	2	127	
4144	9641	A	4436	3	424	
4145	9642	A	4437	1	110	
4146	9643	A	4438	1	110	
4147	9644	A	4439	1	110	
4148	9645	A	4440	1	110	
4149	9646	A	4441	1	108	
4150	9647	A	4442	3429	7466	
4151	9648	A	4443	4048	4181	
4152	9649	A	4444	682	829	
4153	9650	A	4445	163	320	EFEGFNPLKLGEAGWARWLTPVIPA L*ETEAGGSRGQEIETILANTVKPHL Y
4154	9651	A	4446	1122	1446	
4155	9652	B	4447	124	27844	XRSTVPPRISAYERPVPWPGEWNDP RGPGRRASAVVSPREGNWGVLRDP RLQARKPRMVRSRQMCNTNMSVP TDGAVTTSQIPASEQETLVRPKPLLL KLLKSVGAQKDTYTMKEVLFYLGQ YIMTKRLYDEKQQHIVYCSNDLLG DLFGVPSFSVKEHRKIYTMIYRNLV VVNQQESSDSGTSVSENRCHLEGGS DQKDLVQELQEEKPSSSHLVSRPST SSRRRAISETEENSDELSGERQRKRH KSDSISLSFDESLALCVIREICCERSS SSESTGTPSNPDLDAGVSEHSGDWL DQDSVSDQFSVEFEVESLDSEDYSL SEEGQELSDEDDEVYQVTVYQAGE SDTDSFEEDPEISLADYWKCTSCNE MNPPLPSHCNRCWALRENWLPEDK GKDKGEISEKAKLENSTQAEEGFDV PDCKKTIVNDSRESCVEENDDKITQ ASQSQESEDYSQPSTSSSIIYSSQEDV KEFEREETQDKEESVESSLPLNAIEP CVICQGRPKNGCIVHGKTGHLMAC FTCAKKLKKRNKPCPVLTGHIRTEQ PIIILPKKHKKKKERKSLPEEDVAVS SNVFDFTLTKKKVYLNNKLKERSV FKGFQGMGQHWTGFINLDKPSNPS SHEVVAWIRRILRVEKTGHSGTLDP KVTGCLIVCIERATRLVKSQQSAGK EYVGIVRLHNAIEGGTQLSRALETL TGALFQRPPLIAAVKRQLRVRTIYES KMIEYDPERRLGIFWVSCEADTYSR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TLCVHLGLLLGVGGQMQELRRVRS GVMSEKDHMVTMHDVLDAQWLY DNHKDESYLRRVVYPLEKLLTSHK RLVMKDSAVNAICYGAKIMLPGVI RYEDGIEVNQEIVVITTKGEAICMV EHDKEFFHPRYHHREFRFDLSKIPE GEAVTAAEFRIYKDYIRERFDNETF RISVYQGIGSLPARQPYLWASEEGW LVFDITATSNHWVVNPRHNLGLQL SVETLDGQTINPKLAGLIGRHGPQN KQPFMVAFFKATEVHFRSIRSTGSK QRSQNRSKTPKNQEALGWPTMCTD ELSFGDLIVTLQSLFEKRTAAGTRG RPCKKHELYVSFRDLGWQDWIIAPE GYARYYCEGECAFPLNSYMNATNH AIVQTLVHFINPETVPKPCCAPTQLN AISVLYFDDSSNVILKKYRNMVVRA CGCH*
4156	9653	A	4448	2	129	
4157	9654	B	4449	1	462	MSQQYYVRLCQIQPSPSRSVGRENL VLVGDFPDPTELKRVKGRGCAHCG LTDLPEPTAQVLVEQGQDEALWFH NVISEEFGVGVNIFWKHLPSECYDK TDTYGNKDPTAASRAAQILDRALK TLAELPEEYRDFYARRMVLHIQDK AYSKNSE*
4158	9655	A	4450	3	366	
4159	9656	A	4451	1	167	
4160	9657	A	4452	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLVT LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
4161	9658	A	4453	2	252	
4162	9659	B	4454	31	449	MVLSPADKTNVKAAWGKTYFPHF DLSPGSAQVKGHGKKVADALTNA VAHVDDNAQRAVRPKRPCTRTSFG WTRSNFKLLSHCLLVTLAAHLPAEF NPCGARLPGQVPGFCYAPC*
4163	9660	A	4455	2	81	
4164	9661	A	4456	2	81	
4165	9662	A	4457	3	452	
4166	9663	A	4458	1	493	RPRIRHEHRLRENPPWFLFPAAKTN VKAGLG*G*GSHPPSNVAKTLER\M FLSFPTT\KTYFPQLRTLSHGF\SQV* GPRSRRLPDALTKRPWRHVDDHAQ TRCPALSDLH\AHKL\RVDPVNFKLL SHCLLVTLAAHLPAEF\TPAVHAYL DKFLASVSTVLTSKYR
4167	9664	B	4459	208	420	MGNPKVKAHGKKVLTSLGDAIKHL DDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTSLAIHFGIEFTPE*
4168	9665	A	4460	40	534	SRRHGSVSHREAKATIASLWGKVN VEDAGGET\MIRL\LVVYPWPQRSF ASF\SSLFSASAIMGNPKVKA\HGKK VLTSLGDAIKHLDDLKGTFAQLSEL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HCDKLHVDPENFKLLGNV\LVTVLA IHF\GKEFTPEVQA\SWQKM\VT\GV ANA\LSSTYHLNSLPMMQNF
4169	9666	A	4461	2	171	
4170	9667	B	4462	10	351	MAPRTLVLLLSGALALTQTWAGSH SMRYFYTSVSRPGRGEPRFIAVGYV DDTQFVRFDSDAASQRMEPRAPWI EQEGPEYWDRNTRNVKAHSQTDR VDLGTLRGYYRCVSHSL*
4171	9668	A	4463	1	986	
4172	9669	A	4464	3	1282	
4173	9670	A	4465	1	1004	MAVMAPRTLLLLLLGALALTQTWA GSHSMRYFTTSVSRPGRGEPRFIAV GYVDDTQFVRFDSDAASQRMEPRA PWIEQEGPEYWDRNTRNVKAHSQI DRVDLGTLRGYYNQSEAGSHTIQM MYGCDVGSDGRFLRGYQQDAYDG KDYIALNEDLRSWTAADMAAQITQ RKWEAARVAEQLRAYLEGTCVEW LRRHLENGKETLQRTDPPRTHMTH HAVSDHEATLRCWALSFYPAEITLT WQRDGEDQT\HTCHVQHEGLPKPL TLRWEPSSQPTIPIVGIIAGLVLFGAV ITGAVVAAVMWRRKSSDRKGGSYS QAASSDSAQGSDVSLTACKV
4174	9671	A	4466	1090	2175	
4175	9672	A	4467	1	780	
4176	9673	A	4468	59	169	
4177	9674	A	4469	89	134	
4178	9675	A	4470	864	1885	
4179	9676	A	4471	89	176	
4180	9677	A	4472	1	1127	
4181	9678	A	4473	1	405	
4182	9679	A	4474	3	199	
4183	9680	A	4475	3	607	
4184	9681	A	4476	1017	2029	
4185	9682	A	4477	844	1572	
4186	9683	A	4478	1	846	
4187	9684	A	4479	452	1220	
4188	9685	A	4480	1	1254	
4189	9686	A	4481	1	1383	
4190	9687	A	4482	1	1290	
4191	9688	A	4483	666	1606	
4192	9689	A	4484	1	1236	
4193	9690	A	4485	1	1269	
4194	9691	A	4486	719	1175	
4195	9692	A	4487	1	1182	
4196	9693	A	4488	1	1377	
4197	9694	A	4489	1	1335	
4198	9695	A	4490	1	2456	
4199	9696	A	4491	1	1827	
4200	9697	A	4492	1	1011	
4201	9698	A	4493	452	950	
4202	9699	A	4494	1	1433	
4203	9700	A	4495	1	1933	
4204	9701	A	4496	641	2107	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4205	9702	A	4497	1	2582	
4206	9703	A	4498	1	1095	
4207	9704	A	4499	1544	525	
4208	9705	A	4500	2	161	
4209	9706	A	4501	3	452	
4210	9707	A	4502	25	622	EFHRLRENPPWFLFPAAKTNVRA\A WG*RSGAHAG\EYGAEALER\MVLF PPPTPKPYFPELRT*AHGFCPKVKGP TAKKV\AERA*PNAVA\HVDGHAPN GAVPP*ADLQRRTSFRVDPVNFQAP *ATCLLVTL\AAH\LPAEFTP\AV\HA SLGQVPGLSVSTVLTSKIPVKLEPSV GHAFLPLWAFPPAPPPLSCTRTPVG L
4211	9708	A	4505	2	213	
4212	9709	A	4506	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLVT LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
4213	9710	A	4507	2	252	
4214	9711	A	4508	1	466	WSPQTQREPTMVLSPADKTNVKAA WGKVGAHAGEYGAEALGR\IFLSFP P\TKTYFPHFDLSPGSAQVKGHG\KK VADALTNAGAHVDD\MPNALSSPE ATLHAHKLRVDPI\NFKLLSHCLLVT LAAHLPAEF\TPAVHASLDKFLASV STVLTSKYR
4215	9712	A	4509	256	391	NELHAENLKNEDDVDTGLLGFWTL LIISLTAGFSCCSFSWTVTYFDSFEP GMFPPTPLSPARFKK*R*CRHWTIRI LDSTYNIPNCWILLLQLFLDSDLL
4216	9713	A	4510	2	490	
4217	9714	A	4511	1	160	
4218	9715	A	4512	1	150	
4219	9716	A	4513	1	73	
4220	9717	A	4514	2	213	ISPFYHLCQMLKTADVLRRMALWR CRDALLS*GGSSIEIPLFLLYGSRELG LGFCFTGMNHCAQSIYNRF
4221	9718	C	4515	186	365	MFQLLYDSLXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXIYNRF*
4222	9719	A	4516	251	454	GGSSIEIPLFLLYGSRARTWILF*EM AAGRVQWLTSVIPALWEAEAGGSR GQEFKTSLAKRVKPHLY
4223	9720	A	4517	3	192	
4224	9721	A	4518	1	129	
4225	9722	A	4519	23	115	
4226	9723	A	4520	1	1582	GRGWRAVLGWSRRRSGLEPATVGS SMALLFLLPLVMHGVSRAEMGTAD LGPSSVPTPTNVTIESYNMNPIVYW EYQIMPQVPVFTVEVKNYGVKNSE WIDACINISHHYCNISDHVGDPSNSL WVRVKARVGQKESAYAKSEEFAV CRDGKIGPPKLDIRKEEKQIMIDIFH PSVFVNGDEQEVDYDPETTCYIRVY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NVYVRMNGSEIQYKILTQKEDDCD EIQCQLAIPVSSLNSQYCVSAEGVL HVWGVTTEKSKEVCITIFNSSIKGSL WIPVVAALLLFLVLSLVFICFYIKKI NPLKEKSIILPKSLISVVRSATLETKP ESKYVSLITSYQPFSLEKEVVCEEPL SPATVPGMHTEDNPGKVEHTEELSS ITEVVTTEENIPDVVPGS\HLTPIERE SSSPLSSNQSEPGSIALNSYHSRNCS ESDHSRNGFDTDSSCLESHSSLSDSE FPPNNKGEIKTEGQELITVIKSPPPSF C\YDKP\HVLVDLLV\DDSGKESL\IG YRPT\EDSQRNFHEISLSCTQL
4227	9724	A	4521	1	408	
4228	9725	A	4522	2	377	
4229	9726	A	4523	50	326	
4230	9727	A	4524	3	1948	AAAAAAAVPASFGLCSRDPAPPQP ASMSGIKKQKTENQQKSTNVVYQA HHVSRNKRGQVVGTRGGFRGCTV WLTGLSGAGKTTISFALEEYLVSHA IPCYSLDGDNVRHGLNRNLGFSPGD REENIRRIAEVAKLFADAGLVCITSF ISPFAKDRENARKIHESAGLPFFEIFV DAPLNICESRDVKGLYKRARAGEIK GFTGIDSDYEKPETPERVLKTNLST VSDCVHQVVELLQEQNIVPYTIIKDI HELFVPENKLDHVRAEAETLPSLSIT KLDLQWVQVLSEGWATPLKGFMR EKEYLQVMHFDTLLDGMALPDGVI NMSIPIVLPVSAEDKTRLEGCSKFVL A\HGGRRVAYLTETAEF/HTEHRKE ERCS/RVFWGTTCTKHPHIK\MVME SGDWLVGGDLQVLEKIRWNDGLD QYRLTPLELKQKCKEMNADAVFAF QLRNPVHNGHALLMQDTRRRLLER GYKHPVLLLHPLGGWTKDDDVPLD WRMKQHAAVLEEGVLDPKSTIVAI FPSPMLYAGPTEVQWHCRSRMIAG ANFYIVGRDPAGMPHPETKKDLYE PTHGGKVLSMAPGLTSVEIIPFRVA AYNKAKKAMDFYDLARHNEFDFIS GTRMRKLAREGENPPDGFMAPKA WKVLTDYYRSLEKN
4231	9728	A	4525	1	626	
4232	9729	A	4526	66	409	LGLLQVTTTNPPSPPNTYLLKMLFK LRTPPFISHHSFILKNYDIQYFSMRDI DRLGIQKVMERTFDLLIGKRQRPIH LSFDIDAFDPTL\APATG\TPVVGGLT YREGMYIAEEIH
4233	9730	A	4527	1	1257	
4234	9731	A	4528	3	1086	FSVLRIMSLRGSLSRLLQTRVHSILK KSVHSVAVIGAPFSQGQKRKGVEH GPAAIREAGLMKRLSSLGCHLKDFG DLSFTPVPKDDLYNNLIVNPRSVGL ANQELAEVVSRAVSDGYSCVTLGG DHSLAIGTISGHARHCPDLCVVWV DAHADINTPLTTSSGNLHGQPVSFL LRELQDKVPQLPGFSWIKPCISSASI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VYIGLRDVDPPEHFILKNYDIQ\YFP MKDIDRLGIQKVMERTFDLLIGKRQ RPIHLSFDIDAFDPTLAPATGTPVVG GLTYREGMYIAEEIH\NTGLLSALDL VEVNTQLATSNEEAKTTADLAVDV IASSFGQTREGGHIVYDQLPTPSSPD ESENQARVRI
4235	9732	A	4529	1	128	
4236	9733	A	4530	3	126	
4237	9734	A	4531	1	79	
4238	9735	B	4532	214	268	XELEKLVQVVRQLEAEPGLPPVQPV FITVDPERDDVEAMARYVQDFHPR LLGLTGSTKQDEDQDYIVDHSIAIY LLNSDGLFTDYYGRSRSAEQISDSV RRHMAAFRSVLS*
4239	9736	A	4533	23	257	AYLIDDTEAQSRGSQAKATPLEGLR TQPSSRPLGGIKLV*YEVLCLLMTA LKAI/TQIQLPATSHSAARLRGVLPR AIR
4240	9737	A	4534	3	229	
4241	9738	A	4535	1	297	
4242	9739	A	4536	67	552	GPWRFCFSEAVSEPTTVAFDVRPGG VVHSFSHNVGPGDKYTCMFTYASQ GGTNEQWQMSLGTS\EDHQHFT\CT IWRPPRGKSYL\YFT\QFKAEVAGRL RFEYRHGLTFKARILKGESDVPLEN LRNFEV\TKTAVGSQGPGAFPKLTC PKLV\IVAKAS\RTEL
4243	9740	A	4537	2	232	RDGTVHARAAKNRVISVLLPSDLV H*LWEP*PDED*DA*SETGDIDHRV TEESHE*PAFHNFMQESMAQYWKR NNK
4244	9741	A	4538	2	1094	RHPVCLLVLGMAGSGKTTFVQRLT GHLHAQGTPPYVINLDPAVHEVPFP ANIDIRDTVKYKEVMKQYGLGPNG GIVTSLNLFATRFDQVMKFIEKAQN MSKYVLIDTPGQIEVFTWSASGTIIT EALASSFPTVVIYVMDTSRSTNPVT FMSNMLYACSILYKTKLPFIVVMNK TDIIDHSFAVEWMQDFEAFQDALN QETTYVSNLTRSMSLVLDEFYSSLR VVGVSAVLGTGLDELFVQVTSAAE EYEREYRPEYERLKKSLANAES\QQ EREQLERLRKDMGSVALDAGTAKG VFTVDSLSPVLHPSDLILTRGTLDEE DEEADSDTDDIDHRVTEESHEEPAF QNFMQESMAQYWKRNNK
4245	9742	A	4539	710	1053	
4246	9743	A	4540	3	281	
4247	9744	A	4541	30	320	
4248	9745	A	4542	3	115	
4249	9746	A	4543	1	137	
4250	9747	A	4544	3	32	
4251	9748	A	4545	1	135	
4252	9749	A	4546	1	2694	
4253	9750	A	4547	3	544	
4254	9751	A	4548	2	323	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4255	9752	A	4549	1	384	
4256	9753	A	4550	1	1299	MASPVAAQAGKLLRALALRPRFLA AGSQAVQLTSRRWLNLQEYQSKKL MSDNGVRVQRFFVADTANEALEAA KRLNAKEIVLKAQILAGGRGKGVF NSGLKGGVHLTKDPNVVGQLAKQ MIGYNLATKQTPKEGVKVNKVMV AEALDISRETYLAILMDRSCNGPVL VGQPQGGVDIEEVAASNPELIFKEQI DIFEGIKDSQAQRMAENLGFVGPLK SQAADQITKLYNLFLKIDATQVEVN PFGETPEGQVVCFDAKINFDDNAEF RQKDIFAMDDKSENEPIENEAAKYD LKYIGLDGNIACFVNGAGLAMATC DIIFLNGGKPANFLDLGGGVKEAQV YQAFKLLTADPKVEAILVNIFGGIV NCAIIANGITKACRELELKVPLVVRL EGANVQEAQKILNNS\GLPITSAIDL EDAAKKAVASVAMK
4257	9754	A	4551	1	590	RVRTKDPNVVGQLAKQMIGYNLAT KQTPKEGVKVNKVMVAEALDISRE TYLAILMDRSCNGPVLVGSPQGGV DIEEVAASNPELIFKEQIDIFEGIKDS QAQRMAENLGFVGPLKSQVEAILV NIFGGIVNCAIIA\NGIPKACRELELK VPLVVRLEGTNVQEAQKILNNSGLP ITSA\IDLEDA\AKKAVA\SVAKK
4258	9755	A	4552	3	168	
4259	9756	A	4553	3	95	
4260	9757	A	4554	3	354	
4261	9758	A	4556	1	95	
4262	9759	A	4557	156	364	GPVE*KPVEEESRGLLD*GLPGMD WGWVFGKGGDPPLAQSLNCPSFTV SEIIGRDLSGFPAPPGEEPPA
4263	9760	A	4558	1	2523	
4264	9761	A	4559	3	469	
4265	9762	A	4560	3	132	
4266	9763	A	4561	1	2961	MGAASCEDEELEFKLVFGEEKEAPP LGAGGLGEELDSEDAPPCCRLALGE PPPYGAAPIGIPRPPPPRPGMHSPPPR PAPSPGTWESQPARSVRLGGPGGG AGGAGGGRVLECPSIRITSISPTPEPP AALEDNPDAWGDGSPRDYPPPEGF GGYREAGAQGGGAFFSPSPGSSSLS SWSFFSDASDEAALYAACDEVESEL NEAASRFGLGSPLPSPRASPRPWTPE DPWSLYGPSPGGRGPEDSWLLLSAP GPTPASPRPASPCGKRRYSSSGTPSS ASPALSRRGSLGEEGSEPPPPPPLPL ARDPGSPGPFDYVGAPPAESIPQKT RRTSSEQAVALPRSEEPASCNGKLP LGAEESVAPPGGSRKEVAGMDYLA VPSPLAWSKARIGGHSPIFRTSALPP LDWPLPSQYEQLELRIEVQPRAHHR AHYETEGSRGAVKAAPGGHPVVKL LGYSEKPLTLQMFIGTADERNLRPH AFYQVHRITGKMVATASYEAVVSG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TKVLEMTLLPENNMAANIDCAGIL KLRNSDIELRKGETDIGRKNTRVRL VFRVHVPQGGGKVVSVQAASVPIE CSQRSAQELPQVEAYSPSACSVRGG EELVLTGSNFLPDSKVVFIERGPDG KLQWEEEATVNRLQSNEVTLTLTV PEYSNKRVSRPVQVYFYVSNGRRK RSPTQSFRFLPVICKEEPLPDSSLRGF PSASATPFGTDMDFSPPRPPYPSYPH EDPACETPYLSEGFGYGMPPLYPQT GPPPSYRPGLRMFPETRGTTGCAQP PAVSFLPRPFPSDPYGGRGSSFPLG\L PFSPPAPFRPPPLPASPPLEGPFPSQS DVHPLPAEG\YNKVGPGYGPGEGAP EQEKSRGGYSSGFRDSVPIQGITLEE VSEIIGRDL\SGFPETSLEKKPPALKP RETVITLATPAPASALPPFPPFLELV ATEAWGQPLAPLSPSFCLSHCLPLPS PSLGCGPQAWLAALEGLGGKECVE EGGG
4267	9764	A	4562	19	387	
4268	9765	A	4563	1	373	
4269	9766	A	4564	2	343	
4270	9767	B	4565	19	507	MEANGLGPQGFPELKNDTFLRAAW GEETDYTPVWCMRQAGRYLPEFRE TRAAQDFFSTCRSPEACCELTLQPL RRFPLDAAIIFSDILVVPQALGMEVT MVPSKGPSFPEPLREEQDLEALRDP EVEASKLGYGFQAITPYPTTTGWDV CRLIGFCWCPHGP*
4271	9768	A	4566	3	339	
4272	9769	A	4567	3	679	
4273	9770	A	4568	1	139	
4274	9771	A	4569	1	526	HERFETTYFKKFP\GYYVTGDGCQR DQDGYYWITGRIDDMLNVSGHLLS TAEVESALVEH*RLLQEA\AVVGHP HPCEGVNASYCFVTLCDGHTFSPKL TEELKKA\VMRKRLAPFATPDYIQN APGLPKT\RSGKIMRRVLRKICS/VT DHDLGDMSTVADPS\VISHLFSHRC LTIQ
4275	9772	A	4570	537	2357	GVCHQRRLAPQAWPGAGTDSLLLA TRWATGAPGHCCWHLPARHTCGSP GLSPVPQPASAGPPGGLLWERHSRE YIKTWRPR/YFLLKSDGSFIGYKERP/ EAPDQTLPPLNNFSVAGCLGMS\EC QLMKTERPRPNT/FVIRCLQWTTVIE RTFH/VDSPDE/REEWMRAIQMVAN SLKQ/RAPGEDPMDYKCGSPSD/SST TEEMEVAVSKARA/KVGTFGKVILV REKAT/GRYYAMKILRKEVIIA/KVR APGIALASLCGGCVCLQDEVAHTV/ TESRVLQNTRHPFLTALKYAFQTHD RL/CFVMEYANGAVFHLSRERVFTE ERAR/FYGAEIVSALEYLHSRD/VVY RDIKLCAQEKGDTHSP*KVSPSLSSR ITLAPTGTTQVSTVRGTSDP/AVECS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HSGTPHSSWNELQLHTTVWTRLIG YVEGKPHRGAVPRYMGVGQRVLE DN/DYGRAVDWWGLGVVMYE/MM CGRLPFYNQDHERLF/ELILMEEIRF PRTLSP/EAKSLLAGLLKKDPKQ/RL LP/PFKPQVTSEVDTRYFDD/EFTAQ SITITPPDRCECWGPRAESRCLPHAE PSSAAVPDGFPAGPLSPQDAWRGR RGWRRRERAGAAGRTRVRRGHLPE VMPAFLAS
4276	9773	A	4571	64	1537	VTAYHAATMNEVSVIKEGWLHKR GEYIKTWRPRYFLLKSDGSFIGYKE RPEAPDQTLPPLNNFSVAECQLMKT ERPRPNTFVIRCLQWTTVIERTFHV DSPDEREEWMRAIQMVANSLKQRA PGEDPMDYKCGSPSDSSTTEEMEV AVSKARAKVTMNDFDYLKLLGKG TFGKVILVREKATGRYYAMKILRKE VIIAKDEVAHTVTESRVLQNTRHPF LTALKYAFQTHDRLCFVMEYANGG ELFFHLSRERVFTEERARFYGAEIVS ALEYLHSRDVVYRDIKLENLMLDK DGHIKITDFGLCKEGISDGATMKTF CGTPEYLAPEVLEDNDYGRAVDW WGLGVVMYEMMCGRLPFYNQDHE RLFELILMEEIRFPRTLSPEAKSLLA GLL\KKDPKQRLG\GGPSDAKEVME HRFFLSINWQDVVQKKLLPPFKPQV TSEVDTRYFDDEFTAQSITITPPDRY DSLGLLE\LDQRT\HFP\QFSYSASIRE
4277	9774	A	4572	2	423	
4278	9775	A	4573	1	106	
4279	9776	A	4574	3	58	
4280	9777	A	4575	1	191	
4281	9778	A	4576	3	325	
4282	9779	A	4577	3	277	
4283	9780	C	4578	77	292	MVDFCPPCSICFXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXHWSIC IS*
4284	9781	A	4579	645	849	
4285	9782	A	4580	3	140	EANKENREAQMAAKLERLPEKD*A /HLEEVRKNK\ESKDPADETEAD
4286	9783	A	4581	49	605	NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILSP RSKESVPEFPLSPPKEEGFFPGGKFR EN*EAAEERRQSP*SCSS*RQLAEKR E\HGKEVL\QKAIEENNNFQ*NGQK RKLTPHKMEA**RDPREATNGLPKL EPFAEEKDKAH*KKCRKN\KESQRP CPRRDLKPD
4287	9784	A	4582	1	567	VVREPAFSLA/EAQFTARYFSTSSIP NV\NKAPV\RIRRSKHM*QGVTLPVI E\HYHEGTDSL*TALV*ARVGNQLA KLKR\NYAKAVELLVQLASLQTSFV TLDEAIKITNRRVNAIEHVIIPRIERT LAYIITELDEREREEFYRLKKIQEKK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KILKEKSEKDLEQRRAAGEVLEPAN LLAEEKDEDLLFE
4288	9785	A	4583	1	748	MSGKDRIEIFPSRMAQTIMKARLKG AQTGRNLLKKKSDALTLRFRQILKK IIETKMLMGEVMREAAFSLAEAKFT AGDFSTTVIQNVNKAQVKIRAKKD NVAGVTLPVFEHYHEGTDSYELTG LARGGE\QLAKLKRNYAKAVELLV ELASLQTSFVTLDEAIKIT\NRRVNAI EHVIIPRIERTLAYIITELDERV\REEF YRLKKIQEKKKILKEKSEKDLEQRR AAGEVLEP\ANLL\AEEKDEDLLFE
4289	9786	A	4584	166	238	
4290	9787	A	4585	53	203	
4291	9788	A	4586	357	498	
4292	9789	A	4587	262	397	
4293	9790	A	4588	68	422	
4294	9791	A	4589	70	361	
4295	9792	A	4590	259	2603	
4296	9793	A	4591	246	667	
4297	9794	A	4592	25	471	
4298	9795	A	4593	2	3788	
4299	9796	A	4594	1	700	
4300	9797	A	4595	604	1047	SNNRTDNPTSVAYLSKETDVVAKG WPHCLWVVVAVAILVLEAIKIIQGK DFTVWTSHDVNGILGAKGNSWLSD KRLLRYQALLLEGPVLQIHTCVALN PAIFLPEDGEPIKHDYQQIVAQTYVT *EDLLEVPLANPDLNLYTNGSSFV
4301	9798	A	4596	1	1410	
4302	9799	A	4597	510	755	
4303	9800	A	4598	59	411	SWPSDKQTLVVQRGQKMEQANHP DPTDHMSQLMWT/VLPQGFRDSPH LFGQALAQDLGHFSSPGTLVLQYV DDLLLATSSEASCQQATLALLNFLA NQGYK/LSRSKAQLCLQQVKYLCL
4304	9801	A	4599	1	565	
4305	9802	A	4600	·126	492	CNNSMTSLQVRLKVCPRPCRTSM/L PIRII*KLPQVCLDLL*IREGEWDMY PCWAKFPCPYSLKGT*PIAWGILWS FGDFFAY/IPLMQQQKH*FSSQNTRR NEEGQI*WPLLMHSQKPAPLPVV
4306	9803	A	4601	1	342	
4307	9804	A	4602	55	219	LGNKHLLGSIDPRGSWVTGEYIFLR PPIAA*GRQ*DFLPFPELWWTSLNNS WAFS
4308	9805	A	4603	339	1371	ASHPLRGLLCGPSLPNEPCPLLHGT QSHRPLKG*GVRAHSTGLAGSSTCR PLRDPLGEASWAPESAQGL*IHQSA LCI*LKLKPAGQRAKLGDRLDIPDR RKSSTILGRAGDLQPAMPEPPTLSV GSCAAQASPMNPAPCSTAPSPIDHS RAEECGRIARDWQAAPPAGPCGIH WVKPAGLLSLLRDCKYTNRHSVSS SRFANTNQHPASSSGFVNAPIDTLY LANLVGTWRTFVASSGIVNAPISTL SKQTTWLYQSAGCGKESTQASGAQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TGGTSFKSLETTGSISEASSAKHCTE LFSRFTTFNPDSVPSDGVVGDTAGT VWPGVLKGEPCHLGTCYRCVLDPH PTPSESDTIQGIHVQVCYMSTLHDA DVCDTNDPVTHNTKKYIYSTEIFTS NNPELRSEDETVFRALEKWKTSEQT IGEMDFYICNDPHPDSALYQNGLSK MQDTVSLSVFSPSVAA
4309	9806	A	4604	749	1002	QLKKGTNSLLVSKPSPVWIPTGTLT QIMGTGVANIC*PVF*KD*GELGKM NYAMMSTITQGKEENPAFLKWLWE ALRKYTPLSP
4310	9807	A	4605	1	1632	
4311	9808	A	4606	307	543	
4312	9809	A	4607	1	1149	
4313	9810	A	4608	119	409	GDICHHLGLTPVGSHSLLSCSR*QV A*VGAVTAATIGTGILLQQLAFLVC NWLLLSGSSENFPRSALICFKSEREK GTCIQVGPNSPPPTACKGHN
4314	9811	A	4609	1	2433	
4315	9812	B	4610	97	1065	MHAVHTSLLVERTILTTTKERGSTL QYPLRPGAHKGLQDIVKRFKAQALI RKCSSPCNTPILGVQKPNGQWRLV QDLRLINEAVIPLYPVVPNPYNLLSQ IPEEAEWFTVLDLKDAFFCIPLHSDS QFLFAFEDPTDHTSQLTWTVLPPGF RDSPPLFGQALAQDLGHFSSPGTLV LQYVDDLLLATSSEASCQQATLDLL NFLANQGYKTHSRDSDAPVGFTDR HLVATEKIPRGREPLSSLAVYTRGR PTRTGARRTIVSRIRRDFRFFYRYLA QREPPLYQQSLLIHLQLDSQPALSV VIGKVPNVVELTPNFGTAAQV*
4316	9813	A	4611	1	2403	
4317	9814	A	4612	1	2838	
4318	9815	A	4613	1908	4698	SNDRTEDDCGKHPFMSSPP\TEPWV CLIIEGQEIDFLLDTGTTFSVLIPCLG RLSSRSVTIQGILGQPVTRYFSHLLS CNWETLLFSHAFLVMPESPTPLLGR DILAKAGAIISMKTGNKLPICCPLLE GINPEVWALEGQFGRAKNAHPLQIR LKDPISFPYQRQYPLRPEAHKGLQDI VKHLKAQDSVRKCSSPCNTPILGVQ KLNSQWRLVQDLRLINEAVIPLYPV VRNPYTLLSQVPEEAEWFTVLDLK DAFFCIPLHSDSQFLFAFEDPTDHTS QLMWMVLPQRFRDSPHLFGQAQA QDLGHFSSPGTLVLQYSEIAKTLYT LIKEMERANTHLVEWEPEAETAFET LKQALVQAPALSLPTGQNFALYVIE RAGIALGVLTQTHRTTPQPVAYLSK EIDVVAKGWPHCLRTVVAVAVLVS EAIKIIQGKDFTVWTTHDVNGILGA KGGLWPSDNCLLRYQALLLEEPVL QIHMCIAINPATFLPEDGEPIKHDCQ QIIVQTYATQDDLLEVPLANPDFNL YNSGSSFVENGIQRAGYAIVSDVTV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LGSKPLSPGTSTQLAELVALTRALE LGKGKRINVYTDSKYAYLILHAHA AIWKEREFLTSGGTPIKYHKEIMELL HTVQKPKEVAVLHCQSHQKGSARR IFCLTRIPGTRVCKNPHVSLSGISEW PLRDHTPLCFRPKALLAWVHEEICS MGCKDPGWNSLKVSEEDRKMQES LETSRDLLNGFDQNVDNDMDSKVQ AEGASDGDEELIGKWRKGLSMLW KILSIENMMNVWKDGTIKDAIIVIEK AVKAIKPETINSCQRNLCPDVVHDF TRFTTEPIKDIKEIGDLAIKLGIFESS NSTQFLNQFVPDDRLSPHNKLLKFY KPEFYSSYPLVSCLDHYVDQVGARI SMSFCVTTVTEASGSGSWTCGVSQ LKLSYAD
4319	9816	A	4614	1529	2945	
4320	9817	A	4615	3	374	
4321	9818	A	4617	3	112	
4322	9819	A	4618	359	465	
4323	9820	A	4619	3	381	MRILMVGLDAAGKTTILYKLKLGEI VTTIPTIG\FIFVVDSNDRERIQEVAD ELQKMLLVDELRDAVLLLFANKQD LPNAMAISEMTDKLGLQSLRNRTW YVQATCATQGTGLYEGLDWLSNEL SKR
4324	9821	A	4620	395	552	
4325	9822	B	4621	1289	1603	MVVTISPNFSLYRMVVLPAASNPTI KMRICFLPNSREKREEIVRPMAVVA LVMGRSRRGLGRPRAFSFQAPRQT KREGRERAEEERGRQKRLSGPCAD EDPAQE*
4326	9823	A	4622	2	116	
4327	9824	A	4623	156	403	
4328	9825	A	4624	8	2648	WIQYSSTTLPNDWNKRKKKEKKA MLSARAKTPRKPTV/KKGSQTNLKD PVG\YCRVRLGFPDQECCIEVINNTT VQLHTPEGYRLNRNGDYKETQYSF KQVFGTHTTQKELFDVVANPLVND LIHGKNGLLFTYGVTGSGKTHTMT GSPGEGGLLPRCLDMIFNSIGSFQAK RYVFKSNDRNSMDIQCEVDALLER QKREAMPNPKTSSSKRQVDPEFAD MITVQEFCKAEEVDEDSVYGVFVS YIEIYNNYIYDLLEEVPFDP/IKPKPP QSKLLRED\KNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNIKLVQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTRAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPGRRYRNQPRGPVGN EPLVTDVVLQSFPPLPSCEILDINDE QTLPRLIEALEKRHNLRQMMIDEFN KQSNAFKALLQEFDNAVLSKENHM

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QGKLNEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLQQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQNAPPIRLRHRRSRSAG DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDIYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAES\EW\TDV\ETRCSVGC GR*GAGSQLGPGYQHH\AQPKRKK P
4329	9826	A	4625	1	331	
4330	9827	A	4626	142	461	
4331	9828	B	4627	136	906	XPELKPVDKESEVVMKFPDGFEKFS PPILQLDEVDFYYDLKHVIFSRLSVS ADLESRICVVGENGAGKSTMLKLL LGDLAPVRGIRHAHRNLKIGYFSQH HVEQLDLNVSACGTAGHASFLGRP EEEYXGWCDSGVPRMKRFIKAGVP GSCGYAKEGGVTRVERKDFDQYRA LLQGTVSAAKAFL*
4332	9829	A	4628	1	233	
4333	9830	A	4629	1	312	
4334	9831	A	4630	2	119	
4335	9832	A	4631	1	145	
4336	9833	B	4632	78	236	MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSEDKT DK*
4337	9834	A	4633	102	583	IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIAGLQ IGDKIMQVNGWDMTMVTHDQ\AR KRLHQALRRRLVRLL\VTRQS\LQK\ AVQQSMPVLAATTILRLLPAASLYS NATSTLWSPSGFC
4338	9835	A	4634	1	373	
4339	9836	A	4635	3	86	
4340	9837	A	4636	1	204	
4341	9838	A	4637	1	767	
4342	9839	A	4638	20	515	
4343	9840	A	4639	3	391	HEESRSVSQAGVQWRYLGSLQRPP PRFKRFSCLSPPSSWDHRCTTS*LAN F*YLVETGFHHVELLTSSDLPTSAS QSAGITGVSHHAWPWFALNVFKDG CESPWPHNKLEFYTAYYNFFNTGTT LRPPL
4344	9841	C	4640	201	368	MGKSKXAFRXKSXGIVFIQGTFPXE YNXXPRGIKVSQEXNXXXXXCXKI GGEDVX*
4345	9842	A	4641	1	307	RLFFFFETVSHSVTQARVHLSHLGS LQPLLPTFKQFSCLSLPGS*DYRRLL LHPANF*FSVETGFHHVGQAGLEL LTSGDPPTSASQSAGITGVSHRAWP ST

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4346	9843	A	4642	1	310	
4347	9844	A	4643	49	360	DRVSVTQAGVQWCNLGSLQPLPPR FR*FSCLSLLSSWDYRRPPPRPANF* FLVETGFHHVGQAGLKLLTSSDPPT SASQSAEITGVSHRAWPVLSSPQPFF FF
4348	9845	A	4644	2	119	
4349	9846	A	4645	1	276	FFFFFFFFLTQSLTHSVT\RLECSGVI SAHCNLCLLGSSS*LASAS*VAGTT GANHYAQLIFVFLVEMGFHHVGRA GLKL/HDLK*SKVLGLQA
4350	9847	A	4646	2	273	LRQFSLLLPRVECSGAISAHCNLCLL GSSDSPASASRVSGITGTHHQTWLT FFVFLVEMGFHHVGQAGLQLLT*V IRPPRPPKVLGLQA
4351	9848	A	4647	1	106	
4352	9849	A	4648	1	485	SSIDTLGRRVGQPAPGSPGASNHLC CESYPWQLLQPCPVQAGARAELVP VPAHHPGDPVKTEP*RGGQASSGSC TCWGCPTAQAQAQ\PSSPAAPMRK EGPPSL*SERTGRPSRGVTSAGSDG AQPGSA*HSPWPGIVLLSVRYLQETI NHRPGGRPTGFSS
4353	9850	A	4649	1	623	CDLNSQPRSTDGTFDLTVLSNDGVH STVTSNIRVFFAGFSNATVDNSILLR LGVPTVKDFLTNHYLHFLRIASSQL TGLGTAVQLYSAYE/GEQ*NVSFGQ L*SENHNQYVNPSGRSHLLLERHSK RSF/FRQSGVKVESVDHDSCVHGPC QNGGSCLRRLAVSSVLKSRESLPVII VANEPLQPFLCKCLPGYAGSWCEID IDECLPSP
4354	9851	A	4650	1	446	LMLRPRLKLQEPVPHHHLGFQCPSS PLLPP\GPPPHKVV*PLGFQEGGQHS SSLNFVAHSTPAKP/PPGCVCPSLPA SHAHCLSRVIGGVGLRNCTVVPTRG GGSQLPAWLLPSLIVPLIVHQSPVSS LQPIRHDLQPAPGDGTHSSAYC
4355	9852	A	4651	2	388	SHGSYVMIYHDQVEFISGMKHW/FN TKIQTIIY*KNEEKNKMIISTNAENG HDKILLPFMIKTHITLGI*GNVLILIT GIHKQFFWQGQGWGGACGGGRVL LFPQAGVQWWDHSSLQPQPSLNSF SNSSL
4356	9853	A	4652	115	413	LHIYSQPKFRKGTKKIHW*KDSVFH SSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSPMQLIQENTG/IMLQDI GFGKDYLSKTSKAQATKQK*TRKH WEMLQDIGFGKDYLSKTSKAQATK QK
4357	9854	A	4653	3	129	NTLLKKTVSFHQCCWKNWISICRKI KLDSYLSPYTKIKSKLIKNLKVRPET MQLIQENTG/IMLQDIGFGKDYLSK TSKAQATKPK*TRLLSLTIYKNQVK VD
4358	9855	A	4654	1	405	LTLKPNSGFRFPFQVATR*IKYPGIH PAKEVKDLYRKT*KTLLKGITDGPN

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						Q*KTIRGSWIGRINITEMAILPKAIYR FNTTPIKLPMAF\ITQLEKTIQKFIWN QKGAQIAKRILSKKTNSQTSHITVL QTIRI
4359	9856	A	4655	3	448	FFFFFAFLLLGLLHQIPDVSPTGKYT TLLPLMIILMISGIKEVIYIINDMADK IVKEHKTVMTR\LWDTFKWKEVKC GLNTVKALEMGELPSLQDTSPDVFI *QHSNPG*RDKCKTRQGFDREQLLY QCRDILPPRQQAFKLQSLRAQP
4360	9857	A	4656	2	502	KKKKERKRKRTP\IKKWAKDDRHF TGDKIKMVNKNIKICSISLVIS*MQI KAITIHPTRLAKVKCLPRMGR\KGIL FYCWWARKLEQ/SFRKIFIP*NPGVR LLSTNPRKICAPFAKNTRASETWTK LLLAALCVVTPN*KQTNCPSTAGMS NLLASMDHTGRTVSGHA
4361	9858	A	4657	61	364	KTVWFCARVEGQGQNLG*WKPRLP GLKHFPGLSSQ/WNRKLPDGPTNPG *FWNFKKKGGFPLWPKRI*IFGPGD PPSRASKRAGITGITHGAGPRFNFKK WR
4362	9859	A	4658	2	436	KLIIFLYTSNEQREFEIKNTIPFTLAPP KIK*LGTNLTK\WIQELYEKIYKSVM KNIKELNKWRSSYGKGKSSSSSSSS SSSLDIACSWLRRLKIVKISGLHNLI YRFNIVPIEIPETYLVDVNKLIPQFIW RGKRHRIVNKIVE
4363	9860	A	4659	3	480	GSHDFFDKLILKFIW\NSRPRIAKTIL KKKNKVGGLTLCDFKTYYRATV*I KTVWYWD/QIRHI/DQWSRITSPEIN PYIYCQLIFNRYTKTIQ/YGNNRLFN K*C*DMRRVKSDPFLTY/PYIIIN*K MIIDVKAMIMKL/LEGNTGMSLSDF GLRKALDVTTKV
4364	9861	A	4660	362	408	CQVISVLWFYSSVLGWLVWIFCFSL KF*/WKSKRSRQANPILKNKTRVLIL PDIKTYPK\AGVIKPVW*QCS*KVW GEKVWYWQKMTQIVQWDRTESPQ IDN*SLTKEIQWRKDSLFNKW*GNN WTAPFSS/RSLNLNKDLTAVTKIKSK WVTDLNVKHKTINLL
4365	9862	A	4661	93	367	KVWGEKVWYWQKMTQIVQWDRT ESPQIDN*SLTKEIQWRKDSLFNKR* GNNWTAPFSS/RSLNLNKDLTAVTK IKSKWVTDLNVKHKTIKLL
4366	9863	A	4662	123	397	KVWGEKVWYWQKMTQIVQRDRA ESPQIGH*SLAKEIQWRKNSLFNKW *GDHWAAAFSSSSSI*TKTLQP/CTKI KSKWVTDLNVKRKTIQLL
4367	9864	A	4663	2	433	ETADFGPLVLDS/DDDSVDRDIAEAI REYLKAKSGAAQTGAGRGQPGAA QPSRAAGSGSRCKPELSHGSAPTSV CPPK\LVPGSGGGPGSQVRSSED*GS AFPVRASSNDSFEQSIKAEIEQLLNE KR*HATPKCDG\SIDKKPDP
4368	9865	A	4664	94	445	HHQLTLESLGKSKNSPRLSPSLGAC

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						LSCIIWQPAKGQG\SGDGGNWQRG KTAETE/SAAIGGETEWTAKCP*YSC L/GVGPTALTSQPPT/PEAEHPQA/GG TYRDLHPDPTWKTGWCHFVFC
4369	9866	A	4665	52	119	
4370	9867	A	4666	987	1324	VSNTPSARNQGRASSPGNSSPE/SSS ESAPAATANGCDEAHLIPGGKFREP LKGQRGPELGPRPRALGGPRGSI/RP GSGGSFRG*LGGQMLLEPAASPGTQ PSGHLPALCGLSN
4371	9868	B	4667	3888	8771	MRLWSWVLHLGLLSAALGCGLAE RPRRARRDPRAGRPPRPAAGPATCA TRGPRPPRLAAAAAAAGRAWEAVR VPRRRQQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAFTLQ VWLRAEGGQRSPAVITGLYDKCSYI SRDRGWVVGIHTISDQDNKDPRYFF SLKTDRARQVTTINAHRSYLPGQW VYLAATYDGQFMKLYVNGAQVAT SGEQVGGIFSPLTQKCKVLMLGGSA LNHNYRGYIEHFSLWKVARTQREIL SDMETHGAHTALPQLLLQENWDN VKHAWSPMKDGSSPKVEFSNAHGF LLDTSLEPPLCGQTLCDNTEVIASY NQLSSFRQPKVVRYRVVNLYEDDH KNPTVTREQVDFQHHQLAEAFKQY NISWELDVLEVSNSSLRRRLILANC DISKIGDENCDPECNHTLTGHDGGD CRHLRHPAFVKKQHNGVCDMDCN YERFNFDGGECCDPEITNVTQTCFD PDSPHRAYLDVNELKNILKLDGSTH LNIFFAKSSEEELAGVATWPWDKE ALMHLGGIVLNPSFYGMPGHTHTM IHEIGHSLGLYHVFRGISEIQSCSDPC METEPSFETGDLCNDTNPAPKHKSC GDPGPGNDTCGFHSFFNTPYNNFMS YADDDCTDSFTPNQVARMHCYLDL VYQGWQPSRKPAPVALAPQVLGHT TDSVTLEWFPPIDGHFFERELGSAC HLCLEGRILVQYASNASSPMPCSPS GHWSPREAEGHPDVEQPCKSSVRT WSPNSAVNPHTVPPACPEPQGCYLE LEFLYPLVPESLTIWVTFVSTDWDS SGAVNDIKLLAVSGKNISLGPQNVF CDVPLTIRLWDVGEEVYGIQIYTLD EHLEIDAAMLTSTADTPLCLQCKPL KYKVVRDPPLQMDVASILHLNRKF VDMDLNLGSVYQYWVITISGTEESE PSPAVTYIHGRGYCGDGIIQKDQGE QCDDMNKINGDGCSLFCRQEVSFN CIDEPSRCYFHDGDGVCEEFEQKTSI KDCGVYTPQGFLDQWASNASVSHQ DQQCPGWVIIGQPAASQVCRTKVID LSEGISQHAWYPCTISYPYSQLAQT TFWLRAYFSQPMVAAAVIVHLVTD GTYYGDQKQETISVQLLDTKDQSH DLGLHVLSCRNNPLIIPVVHDLSQPF YHSQAVRVSFSSPLVAISGVALRSF

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						DNFDPVTLSSCQRGETYSPAEQSCV HFACEKTDCPELAVENASLNCSSSD RYHGAQCTVSCRTGYVLQIRRDDE LIKSQTGPSVTVTCTEGKWNKQVA CEPVDCSIPDHHQVYAASFSCPEGT TFGSQCSFQCRHPAQLKGNNSLLTC MEDGLWSFPEALCELMCLAPPPVP NADLQTARCRENKHKVGSFCKYKC KPGYHVPGSSRKSKKRAFKTQCTQ DGSWQEGACVPVTCDPPPPKFHGL YQCTNGFQFNSECRIKCEDSDASQG LGSNVIHCRKDGTWNGSFHVCQEM QGQCSVPNELNSNLKLQCPDGYAIG SECATSCLDHNSESIILPMNVTVRDI PHWLNPTRVERVVCTAGLKWYPHP ALIHCVKGCEPFMGDNYCDAINNR AFCNYDGGDCCTSTVKTKKVTPFP MSCDLQGDCACRDPQAQEHSRKDL RGYSHG*
4372	9869	A	4668	1	183	GRDGVLPCCPGWP*SPELKQSA/CL GLPKCWDY/RARATAPGLLFFSYAK ICPCLTSCQYSKC
4373	9870	A	4669	3	462	TYQSFSPSHMPLRGYDVW*TTLFQN P*HG*PGLQRFPLANMLCGPSGSHL VLLKL*RSVTLNHREALICLPPE*YV EPSGTK\CIAGWGETKGTGNDTVLN VSLLNDISNQE*NNQHRGHVR*S*M STDGLQASVGAL***YGGPHSWFIH HRG
4374	9871	A	4670	1	360	ARGPQRSERSSRRPAPPSRSSGS*RC SCIPWPTLLLRGPR*RPL*NARYMKI LASPFQLSHPRKGPRRWH/AGVLSP PPAAPPPSSSSVPEAGGPPIKKQKAD VTLSALNDSDAHSDVVDM
4375	9872	A	4671	70	631	RQRPQRSERYYWRAAPPS*GDKVG PQMASQQPSASLYPYPSTSHITAGS RLGEFHELGWLEV\RWFVVDPLAC RENCETGVWAMGLSVFLSVIHSLT QRSFINTDSVLCHAQRETNVCPCAR EGPCL*PSPSARSQRPRPSPGSRTPQ EKSRPRDAAASSAPRAS*RRRRPPII PLRPLWTLTSWPRAPPHGDAAAAA TREPEFHL
4376	9873	A	4672	93	338	
4377	9874	A	4673	1	660	FRRFRWRRRLH*AGPASSAGGSPGE ASGTMSGELPPNINIKEPRWDQSTFI GRANHFFTVTDPRNILLTNEQLESA RKIVHDYRQGIVPPG\LTENELWRA KYIYDSAFHPDTGE\KMILIGKNGQ AQGFPWNM\TI\TGCMDGRFTGTTP AVLFWQWINQSFNAVVNYTNRSGD APLTVNELGTAYVSATTGAVATAL GLNALTKHVSPLIGPFGPFACVA
4378	9875	A	4674	1	387	FFF*RWVSHSVAQAAVRWRNHGSL *PKTLGPK*SSH/CQSP*RAWDS*AH AHYHPA*FLNFFL*RQGPHLSM\FPK MVLNS\RPQAVPPT*ASQSDGITGVS HHTLALKV/CLFKMKYFE**TEKGI

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						HFKRTK
4379	9876	A	4675	3	383	GQLQARPPAPAAADCPPWTLRGSA LVPWLVPWRKASPQLSPGSPECP*A PSARPQDPPRPAGQIQDRASEHAAR GGPCGVLRADGALPALPPDRARPQ VCGRGEVAARARW*RSSGRRGTKR RNGE
4380	9877	A	4676	490	1013	WASCSSSREYQCCFQTVPPGFSRVM KFFTFFPGSCKHFPAPL\PAPQACTSF GLAGLPPNALPLILVPAPPA/SSLAN PQLVQPPV\PGLVPRPSRSRCSAA/RP SA/RLARPPETPAR\PRAPSSAPRTRT PS*GRARSGGSAGNAPSARRTPQGP TRAACSLARILDLASGSWRVLRP
4381	9878	A	4677	1	447	KKFVIPDFEEFTGHVDRIFEDVKELT GGKVAAYIPQLAKSNPDLWGVSLC TVDGQRHSEGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIVVS SLIKMDCNKA*KFDFVLQYLNKMA
4382	9879	A	4678	3	284	QLGQYGETPSLLK/IKIRIQKVAGHG GRHL*SQLLRSLRQKNLLNP\GGRS CSEPRLRHCTPAWVTERDSVSKKK KKKKEKERKKKKAGCGGSRL
4383	9880	A	4679	122	196	CWFENVNSKSGFWVLF*FKAKLVN
4384	9881	A	4680	2575	2786	ADTESITL*FYHFFFFFLRL/DSVAQA GVQWCDLGLLQV/LPPGFTPFSCLS LPSSWDYR/RPVITPS*FFVFLVEM\G FTALARMVLIS*PCDPPVSASQSAGI TGVSHCAQPTFIPK
4385	9882	A	4681	3	512	YNQKVDLFSLGIIFFEMSYHPMVTA SERIFVLNQLRDPTSPKFPEDFDDGE HAKQKSFISWLLNHDPAKRPTATEL IKSEL\LPPPQM\EESEL\HEVL\HHTL\ ANV\DGEGPYRTIDGPRSFRQRISPAI DYTYDQRHS*KGTSSIRA\AKLLHL VRETMIRICTRHGACQT
4386	9883	A	4682	1	382	EESILGEVGEALTSAGEELKIDRFF*I VEGLRHNSSQLNVTSMQLINALDTS PDDLDFRLHIINEFMRCGLKEILPHL *GIKNDGLDMQLKDFDEHNEEDLL ECI\HRLEDIRAELDESYDVHNMLW S
4387	9884	A	4683	1	472	GIMLPDLK\LYDIAMVAKSAWYWH KNGHKVLWNKMAQN/HIYGQLVF VKVPKYTQWGKGSLFNEWNQE/N/ WISACRRMKLDPYV\STKINSKWIK AYTIR/PETVKLLEENIGKKLIDI/GP G**FLALAPQTQATKA*IDKWDFIK VKTFCTARETVNTEKRH
4388	9885	A	4684	182	345	RFPLCSFPPTLPCEGICFPFA\FCHDC KFPEAFPTRLPVEPAEL*VNSTSSLH KL
4389	9886	A	4685	205	395	VNLGIFGKNGAPPG/PEGRGGILGHR NPPPRGLNK*PPLTFQGTGTPGSSSS S*VNLGIFGKNGAPPGGQGGPKTPG PKEWAGLAPQKGGTTGLDPLGPPK

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						KGFNNHPGGIREFPGN
4390	9887	A	4686	35	389	NLFYKVLQSAGFFSMDHEDDVDFL ARFSQLVTGKRQSLIVSWTT*IQNG DIKNAQEALEAAETRMALTLR*LAP DDGTSSKI/LGFCCDYVQILKHL\DQ QKAGAAAIMSVATKELMMKT
4391	9888	A	4687	3	547	GGAGRRAWAGVGGAPGAGGGPAE AGAAAEEGAEHRGDGAVRAGAGG GRRYRPRRVQDPGGPAE/G*TWPPS PSSRCSSPCVPGRG*/PSEPQDPAAV SLPTSSVPETRGPAPAGPIRG\PAPGL RCQP*EARPGCVYWLISGGWCSPLF PWKLPGPRRPKQL*APRAGPCRPSL PCRLATGHDF
4392	9889	A	4688	65	414	WKCADTNVAQGPRVQQVLQLRGT PIPNHCALCLLREKQRQLCPRGSNG P\AERSKPRRIQPEDATPAQALPRLP KGGGPGKSPTRGKHLGWGRDLFAS LSPAKATCLPPSIDNKPF
4393	9890	A	4689	75	787	HVAFASGQRCNKSLPTPKVVPRVG LFPRPRPPWAALVALGLAWHPLAGI PRGCCVPHRHNAPPEGKRLPFVSPS GHRARSTWAETRPQGPRGSLASLCP AHMDLSIWKTARGATFSFQQGPPG SWRGQT/RGPVSPLRPARPPP*RPDK DGGGGS\PDQRAGRTRKAEVGGCL ASMRPPPAPLT*TRRGR*RRPAPAP ARTAPSPRCSAPSSAAAPASAGPPP APGAPPTP\PRPRPYALRR
4394	9891	A	4690	8	382	QEYWE*LYAYTF*NRDELDEFFDRH ILPNFTQEEYTT*NNPVSVKEIEFVI/ NNISTPKKNPK*TSDPDDFTSKFC*T FKEELIPVLYKHFQKIVEEEVLPHLF CELSITFLLKLDRRCEVRRLHR
4395	9892	A	4691	2	389	NRKRIELTRKVLFELKHMRDVQNE HLTRFVGACTDPPNICILTEYCPRGS LQDILENESITLDWMFRNSLSSDIC* GMLFIHNAA/IC*HGNLNSFNSVLIR DLSRFN*FSFSSESPVNCIQIIVIIISP
4396	9893	A	4692	2	544	TKAPKYIKQTLIDPKGEVDYNMIIV G/DANTPLSKTDRSSIQ*INKETVEL N\HILDLIGLTAIYRTFHPTATE/YFFS SAHGTLSRINYTLGPKPGCEKIVKH RNYIKYPFLNTIELEINNKRN\SENT NTWKLNNMFLKD*WINEEIKKEI*K LLETNENGNTM*QNLWDMTKAVL RMKFIT
4397	9894	A	4693	1	373	MPHSVPG\LMSPGIIPPTGLTAAAAA AAAATNAAIAEAMKVKNIKLQAMS NYHASNNQHGANSQHGDMISRVAL DLPLSILPNLYTMPLVLQHSHPTYN HLTYS*LHNLQTIP*INLDQRAPSLP
4398	9895	A	4694	185	417	NSELNGKEAALQ/IMILEREIGVEKA LNVQKGRVSESLKLLANRPGMVAH ACNPSTLGGQGGWV\VIRSGVRDQP *PHG
4399	9896	A	4695	88	432	TDLFLFVCLRLS\LLSVAQAGVQWF

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						DLSSPQPPPPRFKRFSCLSLLSSWNH RCTPPRLV/N/FFVFLVEMGFTMLAR MVSIS*PCDLPTSASQSAGIT\GINCR TQLTY*F*KFSVDSL
4400	9897	A	4696	3	390	YRIPYYVSTDCENLLKRFLELNPVK RLTLKQIMNDRWINARHEEDELKPF AEP*L\DILDQKGIYIIGGMGYSQEEI WESLTKMKYDEITATYLLLGRKSS HLDASDSTSSTNLSLAKGRPSTDFN NSTG
4401	9898	A	4697	289	365	SPRLGLPKCWDYRHEPPHPAAFH*G CVLFIFYFIFLKQEL/NSLTQAGVQW RDLSSLQPPPPG\FK*FSRLSLQSS*D YSCVPPRLAFCIFFW*KRGLTMLTR LVSNS*PQ/CDPPALASQSAGITGMS HHTQPHSIVL
4402	9899	A	4698	33	397	NAYNQLKVCASSSPWLFFCANFSSY YFYDSHNVIQG*NMTYCT/VM*YLL ITGSLSAHLKNMSLKRIMKSYRSGA ESATEEPFTILYESQFSVGGNELDFQ VKTLSLPEVVIVHGSQDNNATA
4403	9900	A	4699	2	371	LNTVIANGVAMASRPYQPTHVNVH IHQESTLTHLLKAGGTLKKTLFHPG DTVSSTATIGYEQLALWVTQILLGR *E/CVILECVLILGPWTALSASRCAF WAESVEIVPRAGAIVHDKQPVKLA
4404	9901	A	4700	3	441	GFEDKVFYVWFDATIGYLSITANYT DQWERWWKNPEQ/ALGAEDNYTL VSHLIATEYLNYEDGKFSKSRGVGV FGDMAQDTGIPADIWRFYLLYIRPE GQDSAFSWTDLLLKNNSELLNNLG NFINRAGMFVSKFFGGYVPEMVLTP
4405	9902	A	4701	2	375	CITRDLKWGTPVPLEGFEDKVFYV WFDATIG\YLSITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLAKLLDLKKQLA VAEGNPLKPLKARRKSKRPWLIESH FNR
4406	9903	A	4702	1	3093	
4407	9904	A	4703	2	2717	GEMRLFVSDGVPGCLPVLAAAGRA RGRAEVLISTVGPEDCVVPFLTRPK VPVLQVDSGNYLFSTSAICRYFFLLS GWEQDDLTNQWLEWEATELQPAL SAPLYYLVVQGKKGEDVLGSVRRA LTHIDHSLSRQNCPFLAGETESLADI VLWGAQYPLLQDPAYLPEELSALH SWFQTLSTQEPCQRAAETVLKQQG VLALRPYLQKQPQPSPAEGRAVTNE PEEEELATLSEEEIAMAVTAWEKGL ESLPPLRPQQNPVLPVAGERNVLITS ALPYVNNVPHLGNIIGCVLSADVFA RYSRLRQWNTLYLCGTDEYGTATE TKALEEGLTPQEICDKYHIIHADIYR WFNISFDIFGRTTTPQQTKITQDIFQ QLLKRGFVLQDTVEQLRCEHCARF LADRFVEGVCPFCGYEEARGDQCD KCGKLINAVELKKPQCKVCRSCPV VQSSQHLFLDLPKLEKRLEEWLGRT

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPGSDWTPNAQFITRSWLRDGLKPR CITRDLKWGTPV\PLEGFEDK\VFYV WFDATIGCLS\ITANYTDQWERWW\ KNPEQVDLYQFM\AKDNVPFHSLVF PCSAL\GAEDNYTLVSHLIATEYLN YEDGK\FSKSRRVGVFGDM\AHDTG IPPDISRFYL\LYIRPEGQDSAFSWTD LLLKNNSELLNNLGNFINRAGMFVS KFFGGYVPEMVLTPDDQRLLGHVT LELQHYHQLLEKVRIRDALRSILTIS RHGNQYIQVNEPWKRIKGSEADRQ RAGTVTGLAVNIAALLSVMLQPYM PTVSATIQAQLQLPPPACSILLTNFL CTLPAGHQIGTVSPLFQKLENDQIES LRQRFGGGQAKTSPKPAVVETVTT AKPQQIQALMDEVTKQGNIVRELK AQKADKNEVAAEVAKLLDLKKQL AVAEGKPPEAPKGKKKK
4408	9905	A	4704	180	490	VENGNNSLTIMNRRARQKINKE\TA DL*NTMNQMDLTDIDGTFYPKAEY TFFSSKCGTF*RTDHMLGHKTS\LD KFKKIKVIQNYLFNHNGVKLEINNS KKMRKF
4409	9906	A	4705	2	405	KNLNNRLFIFP*IKEEIKRQIRK*FEW NEKEKTIYQNLWDAPKAKLKEKCI VLYV\KEETSQITDLSFHLKTPEKEE HVKPKVNRRMEIIRIRAEIIAVKYRK PTETNETKSWSFENFSKIDTPLIKMI RKKKVD
4410	9907	C	4706	217	486	MDDPRGHASPVTRTQKPQASRLLV GLRAGGLSWGHKWGRGKPPRGRV PAAALGAAVVAAMASPDPWAPGP KQPGRWADLAALLLCGLRPA*
4411	9908	C	4707	13	216	MLYWDCKRYKVKDKTQAWDFAG NISVKGAELSQTRAASGPRRQAQVT FSVWRGGLQVMAEEGRVDVC*
4412	9909	A	4708	132	1424	VKHGPQGGPRRQAQGDIQVFGVGV LPGEWPEEGTQKGGPPLKTLGT\GD GDKIGEPPTRAP\RFRTGQPGPRDGL VGPGGELAKPWGPPRGLGPASCPP GNTPLPARPEY*HLGWVGCP*RMG QGNLGVPSK/PVFGSSGPNVGSTNC DNFGSFGLSVPMFPNGPIQRALFEG DLWDLGRTGHGTTPGGQCKPLSPG PKKLQGL*TC*SSLALQG/RLSLGAQ SGGRGKPQESESPCPNP*APPVVGC YGITRPVGFRGPSQPG/LMGRPGSSS ALWA*NPPELPNCPGL\PQPCPQEVP QSFGPPGVRGRGLKGGQDCHRGRG EGSSKCAQGGHPAPA*WNPLVYTP ASPFPFRPASGKPRS/RPSCGLRAPS* HLRRPCLTPPFRPQGLLGSSPCPQKP APDSGLLHSPLTSPRGLSGQCNPRR LHPQLNQSNRDR
4413	9910	A	4709	1	340	RHEERTTGILTSVGLASDTSLICVIE DFFDTALIISRSSSEGKIQMLDSFLLS L*LLVTEETVNHLLQQEDRPCMDTL DCG/LQVAISEALRRLTTSKSRDDLV

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						HIWYDDESIV
4414	9911	A	4710	12	398	TYLDLPLPGFCIYDF/VPPFSSSECFIF VFMVCFFLAFILSFSSSSSPNSFFDLF FLALPQLPTLRGLFV*ALFQILSWVV FPVKFSLGCVFYLFFQFIFKQLAFFH HV*ETFSPVFLICKYWDD*TYFS
4415	9912	A	4711	111	453	YPFIIITFNTLGVAGNCL/KLTYTI** MPTANIILKKLKAFSLR*RTR/H/GCP QSI*ARRII*DIQIAKEDVKLYLFTDD MILYVENPEESTQKDLL\NKVNKVS GYNINMIIRCISM
4416	9913	A	4712	1	184	SSRDILLCTDIASRGLDSTGVELVVN YDFPPTLQD\ELAARRRRSLPGLASS VKEPLPQAT
4417	9914	A	4713	1	1630	MALTRPVRLFSLVTRLLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLPRPVLVRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLEPRVLHALQEAAPEV VQPTTVQSSTIPSLLRGRHVVCAAE TGSGKTLSYLLPLLQRLLGQPSLDS LPIPAPRGLVLVPSRELAQQVRAVA QPLGRSLGLLVRDLEGGHGMRRIRL QLSRQPSADVLVATPGALWKALKS RLISLEQLSFLVLDEADTLLDESFLE LVDYILEKSHIAEGPADLEDPFNPK AQLVLVGATFPE\GVGQLLNKVASP DAVTTITSSKLHCIMPHVKQTFLRL KGADKVAELVHILKHRDRAERTGP SGTVLVFCNSSSTVNWLGYILDDHK IQHLRLQGQMPALMRVGIF\QSFQK SSRDILLCTDIAS\RGL\DSTGV\ELV VNY\DFPPTL\QDYIHRAG\RVG\RVG SEVPGTVISFVTHPWDVSLVQKIEP AARRRRSLPGLASSVKEPLPQAT
4418	9915	A	4714	79	410	IVYWVEVENRDHYAAYLGWEEAP YSDRAYAPQEKDLGPMDIRIGLL*K NWIPLQDDLYPVDMLHTSVG*EMEI LNNCRNQGV*RMSKDRRETLETYQ QL/L*LLQTSPLYLA
4419	9916	A	4715	185	449	TTILAWGDYLSLENSRSGPN*L*LLS GCTVQSFGLDWNGLLK*DSLTRLP ALCSLQLGRK\VETITIIYDCEGLGL KHLWKPAVEAYG
4420	9917	A	4716	154	364	MWRWFSLPPPFSLAGVELAPPVSRR SPRGP/TPYGLPRVPLWPLHSTALYC P\PSPRTSAPFTPHPLPKLRG
4421	9918	A	4717	9	1805	SPATSP*ETAGPVKRSRNGSSPAADP EALSPPTARLQRVTVPPI*LNGQLSS PLHFAAGGGHAEIVQILLNHPETDR HITDQQGRSPLNICEENKQNNWEEA AKLLKEAINKPIEDPLAILILFDEAR YNLLKGFYTAPDAKLITLASLLLQI VYGNYESKKHKQGFLNEENLKSIVP VTKLKSKAPHWTNRILHEYKNLSTS EGVSKEMHHLQRMFLQNCWEIPTY GAAFFTGQIFTKASPSNHKVIPVYV

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						GVNIKGLHLLNMETKDFQYFQYYV D
4422	9919	A	4718	200	529	EDVSKPVPWTLNGSCTSPLISHSDN QKCPPYFPVIPAMGNPENIEDAYVA VIRPKNTASLNSREYRAKSYEILLHE VPIEGQKKKRERKFYWKRNFKATV K*HKAYWIT
4423	9920	A	4719	177	321	QTCSMDTKWQLYISPHQS**QPEMP SIFSSDPSLQCVCLIICKRLLS
4424	9921	A	4720	166	627	MWRWFSLPPPFSLAGVELAPPVS/S KDTERSHPYGLPRVPLWPLHSTKW VGQSPGEGGQGPSPLSHSSFPPPRHS SPAQLPVAEKPSVAKRKPS*GFPRA PTRAPKAQVSGVGDPPAHLLFTVLP SPRTSAPFTPHPLPKLRGPRSSKALA FHSA
4425	9922	A	4721	3	610	STFNNEP*PEKQEQNKHKIRRKQIIK IRA*INKIE/TKNQCKRTMKQKVAFF QKLNKTDKPLARLRKKRQD\KIRNE KDITTDTAEIQRIIRGYYEQLYANKL ENLEEIDNS*THTTY*DLDQEEIQNL NRLITSNKVEAIIKSLPVKKSLGPDG FTAEFYQTFKEELIPILLKLF*KVEEE RVLPN*FYEASITLMPKPDKDT
4426	9923	A	4722	1	454	LAHCNICLLGSSNSASVSQVAGITG GCHYTQLIFLFLVEMGFHHVGQVG LELPTSGDLPALASQSVGITAVSPLC PTRIIFFEAESCLCWPGWSPNPGLKQ SPCLGFP\KCWDYQPDLTMPS*FYL LELEIKFGVHVLWKSFLIKIENYYC
4427	9924	A	4723	1	318	KEECNKEEKESREKK/NEKEKIE*KE EEVRKEEKKSLNKDKDKKRRKREK GEGRKKEEGILKVKKDGNPSNGHA RMPKER*LYDVRGTKPHSSDHGDT AIFQTCIL
4428	9925	A	4724	42	200	LICT*MLIVALLVIARNWKQIRC/SST /DEWLNKLW*IPMEYY*AIEKEPTIG TC
4429	9926	A	4725	50	403	VVYHMVMVLLKVVICHHFLTLFFS FRSLILYLFFILFMISLYLSCFLYNFL FIPSSSIFSIICFLMIIVLI*FFFYALFIIII FNPIILYLN\YLLSLFLIESLFDYYLCL ISFVIFY
4430	9927	A	4726	3	282	VQGQEPLTASMLVAA/PPQEQKQM LGERLFPLIQTMHSNLAGKITGMLL EIDNSELLHMLESPESLRSKVDEAV AVLQAHHAKKEAAQKDSKAK
4431	9928	A	4727	780	1249	LVVFMSIPLCSSTHPSILQGLKLVPL EQGQPPPLLFHIVRCSDIEQALNHH QVLSFPQC*PTAFPGSQAPQPAVHV QGQEPLTAS\ML\AGAPPQEQKQML GERLFPLIQTMHSNLAGKITGMLLEI DNSELLHMLESPESLRSKVSWGSDP AASVLM
4432	9929	A	4728	510	2771	NLEPSHQDRGEVQSRGEGRIVRRAF CLRCCGRGSRPPPPVSVPSPSPPTPA RPRRAGATCEPARARAPAPKAPLCP

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						AAGPIRSPLAGLGVVGGGEMNAAA SSYPMASLYVGDLHSDVTEAMLYE KFSPAGPVLSIRVCRDMITRRSLGY AYVNFQQPADAERALDTMNFDVIK GKPIRIMWSQRDPSLRKSGVGNVFI KNLDKSIDNKALYDTFSAFGNILSC KVVCDENGSKGYAFVHFETQEAAD KAIEKMNGMLLNDRKVFVGRFKSR KEREAELGAKAKEFTNVYIKNFGEE VDDESLKELFSQFGKTLSVKVMRD PNGKSKGFGFVSYEKHEDANKAVE EMNGKEISGKIIFVGRAQKKVERQA ELKRKFEQLKQERISRYQGVNLYIK NLDDTIDDEKLRKEFSPFGSITSAKV MLEDGRSKGFGFVCFSSPEEATKAV TEMNGRIVGSKPLYVALAQRKEER KAHLTNQYMQRVAGMRALPANAI LNQFQPAAGGYFVPAVPQAQGRPP YYTPNQLAQMRPNPRWQQGGRPQ GFQGMPSAIRQSGPRPTLRHLAPTG SECPDRLAMDFGGAGAAQQGLTDS CQSGGVPTAVQNLAPRAAVAAAAP RAVAPYKYASSVAAALILPYSLCRH PS/PAVHVQG\QEPLTASMLAACNPP /QKQKQILGERLFPL\IPTMH\PNLAG K\ITGMLLEID\NSELLHMLESPESLR SK\VDEAVAVLQA\HHAQERSCPEG GRCCCCYLLDPRKTDSKAK
4433	9930	A	4729	7	365	LYTRHPPSPSCIMTACFGSHIRYRSD *VPTPVLRPAVIRSVGGGDCSERLG LRPRPI/PELGPHTPTRPPPPPWQNV QRADPVAVTPCRSREGSQAEPLPRG RGAVSSSTTRPGLPAPNRP
4434	9931	A	4730	1	1520	AEGACGPRQPNKGAGAPPQGPATH LPGPRSGLSSTATMTANGTAEAVQI QFGLINCGNKYLTAEAFGFKVNAS ASSLKKKQIWTLEQPPDEAGSAAVC LRSHLGRYLAADKDGNVTCEREVP GPDCRFLIVAHDDGRWSLQSEAHR RYFGGTEDRLSCFAQTVSPAEKWS VHIAMHPQVNIYSVTRKRYAHLSA RPADEIAVDRDVPWGVDSLITLAFQ DQRYSVQTADHRFLRHDGRLVARP EPATGYTLEFRSGKVAFRDCEGRYL APSGPSGTLKAGKATKVGKDELFA LEQSCAQVVLQAANERNVSTRQGM DLSANQDE\RPTRRPSSWRSTATPKS VPSVPTRASTGR*RPPGACSPPPPAR MPAATLTSSGVTGASH*GRPMASL* PPRRMGSWPPRWRQQGTQSSSS*SS STAPSSCSAGSMASSAAARSRAPWT PTAPAMTSSSWSSTMAPTTSKTPQA NTGRWAVTPRSPAAATLLWTSSSSS ATITRWPSRWAGAT
4435	9932	A	4731	131	677	PSSLS/CDIFLRSPISTPSPSPLPRTPTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTPSTGSPTNKISTASQISQ GTGSPVPKIHGSSFVTSTVKVIIKQE

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						PGEAPHVPATGAASQSPLPQYVTVK GGHMIAVSPQKQVITPGEGIAQSAK VQPSKVL/GQIG*CLPTLARADLLYS VC
4436	9933	A	4732	131	362	PSSLS/CDIFLRSPISTPSPSPLPRTPTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTPSTGVY*IHICTI*RV
4437	9934	A	4733	1	4461	
4438	9935	A	4734	2	614	STTTERENYRPIFLMNTDGRILSIILP SQI***MKKIIYHDQVGFIPGMQRWL NVHK\TMHVIHHINKMKGKNYLIIS ADAEKSLGKTYHCFMMKTLNKLGI EGTL\NIRKGIYD*STANILLTGKN*K AFPLRTGIRQGCPLSPLLFNTVWDIQ AKVIRQDKQIKGIENGQEEVKLSHF ADDIILYL*TEKPKDSTKKLLKWVN
4439	9936	A	4735	164	613	NLNMEATGTDEVDKLKTKFISAWN NMRYSWVLKTKTYFSRNSPVLLLG KCYHFKYEDEDKTLPAESGCTIED\T *LREM*KNFRKDSISRIWLTYREEFP QIEGSALTTDCGWGCTLRTGQMLL AQGLILHFLGRAWTWPDALNIEKLE L
4440	9937	A	4736	40	359	
4441	9938	A	4737	4274	5256	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNIILPKFNHLCTHTHTHTHLTLFST YLKNDRDKTIMCKLSLIG*L\ESLEF GGSGENVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWLDLGT LSV
4442	9939	A	4738	133	359	LLNFMLLFHRYYALKVSYFKSSLDR KLLELLWNKYWVNTLSSSSLLTVS/ DYTCKECI*ILSKLHSRLISETLFHRK
4443	9940	A	4739	1	353	NWTL*TLKKIFSLKDAIKRIKIQSVR WKKIFAKHTSDKGVES\NIYKELS*I NKASSSSSSSSSS/HSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSYHYTSIRVA KMKKTDYVTSW
4444	9941	A	4740	1	375	LVPKRA*YWHKNTSSSSSSSSS/PSS HLHIYSQPKFRKGTKKIHW*KDSVF HSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSPMQLIQENTG/IMLQD IGFGKDYLSKTSKAQATKQK*TRKH WEMLQDIGFGKDYLSKTSKAQATK QK
4445	9942	A	4741	1	296	FRRSL/DSVAQAGVQRRHLGSLQAP PRGFTPFSCVSLSASWDHRSPLPRPA NFFVFLVETGFHVLARMVSIS*PCD RPT\SGFQSTGNTGVSHRTWPLLL

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4446	9943	A	4742	3	380	FLEEYNPPKVSQEEITSSSSSSSSSS SSSSLSSDIES/VIKNTSSNNNKKNPG PDGFTAKFYQM*KDELISTLLKIISK/ IFHSNSFCE*QTTR*FAISITWRAKPD KDTPQKEPYRLISLINIHSC
4447	9944	A	4743	3	369	SFTLIKKTKDIIRKANYKTMSLRKIA AVILNKILAN*IEH/RIKRIIHHNQIRF I/SGTQVWLNI*K*INVTHHINRLKK KNYMIILIYEEKTFDKIKHPFM/IK/V LSKLGTENFFKLIKHIWRKI
4448	9945	A	4744	70	345	KVWGEKVWYWQKMTPIVQWDRT ESPQIGN*SLTKEIQWRKDSLFNKW *GNHWTAPFSS/RSLNLNKDLTAVT KIKSKWVTDLNVKHKTIKLL
4449	9946	A	4745	3	345	KFNNLDEMDKFADRQKLPYLAQEE RQNLN/*PYLLKNLNVQNLPISKTSA PDELICKFYETFKNEIILLLCSLFQK MELSQHIHDSNLTLTQ\KI*K*YRTE ENYRDISLINTYAK
4450	9947	A	4746	35	355	PHPPWWSLSSSPPSQHSFLPSPAYM PSPSGNSM/CYLSPSRGM*APSRQGP SSFHQLCPKCLKGCWARHMPSK*G WNGNPFPVSLNYPWARNRPSLLTH FVMWEAPRP
4451	9948	C	4747	27	416	MMKRLGMFNIQHCKKLSSWVLLM KYLGNAPPSSSCLMRGNYSTWKMN SPTISSPSSWENEDRRSASLHLPKLSI TGTYDLKSVLGSTGASLKVFQQWG AGPLPGFTEGGHPXKVFQGPCIKAV LEPFDE*
4452	9949	B	4748	5	763	MPSSVSWGILLLAGLCCLVPVSLAE DPQGDAAQKTDTSHHDQDHPTFNK ITPNLAEFAFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEAFTVNFGDTEE AKKQINANGTRPFEVKDTEEEDFPR GPGDHREGAYDEAFRHV*
4453	9950	A	4749	11	368	GLKSLIN*LLAVYPREQTTLEEVMR DPWVNS/GSGVAFDN/TE*QILDHLN PETTQLLVAMGFQADNLSVAVREQ LFSYAMATYLDLEHTLLKKRSTIRS QTLPPGDPTWPLYIEVCTFRLS
4454	9951	A	4750	175	349	PSVAGRPRRKGGGRQPAQTRAVGI AGTEPPLYYLGLWGPVGVDQG*QP ASFPGPPQPVPKAPSNTKEA\SPSNA HSSSLGRLPSSPLPPRPASNTGSLSPR QGTMTTL*GATHLPQHSD*EESTRE SPPPTLEQPLPPSVQLIRMPCPPLPVT Q
4455	9952	A	4751	2	354	ENCQINNLRFHLRKPKKEEYTKPTA SRRK*IVNIRIERNGIEQKNNRTSSSS SSSSSSSSSSSSLTFR*MDGRRSSSSS SSSSSSSSSQ*QRK\KTRLIKI*NERG DITADLTEIK*LLILQKLNNY
4456	9953	A	4752	121	363	WRDFKTKTVIRAK*GYLIITG*NHQ

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						EDTTVINMYA\PKTAPKKYMKQKL TDWKRAV/DSKTTAGDLNILLLIMD KTKQKINRV
4457	9954	A	4753	178	439	GPALINALLKWRIPSGEDREP*GRD WEKEKE/R*LEEGRERGGKGEGGK RRNKGRKEGREERGKGEREEGYIM CIHGIGNRSLAVLGA
4458	9955	A	4754	193	355	GLFSIEEH*HDSTHLGINTL\LISRLFI EK*LLKRVYQVTQACELYAWNNPN DQCLPPPLVRPVQHRGAYPGEDWQ IDYTQMPPCKGFKY*LVFIDTFTVWI EAFPTKIEKAIKV
4459	9956	A	4755	3	227	NIKIGKEEVKLSLFAGDV\YLEKPKD STKKLLLELI/NFSKVAAY*INIQKSVA FLYANSE*SEKEIRNIIPFTIAT
4460	9957	A	4756	115	487	CSLCFVAEWSPWCGWTQLIYPW*E/ ITHSPVHTQRLGLETHRTAEMRLFS FSLFFFLRQSFALVTQPGVQRCDLG LLQPPSPGFK*FSCFSLPSSWDYRHA PPRLANFVFLVQTGF\SMLATLVSN
4461	9958	A	4757	2	436	GTEAEQPSYQPGLELPQGDQEEP\G LAGKTGLGPRFPRTTGGSQGTLLEV EGLSHSPFQSPGIPGEFEKARKIL*A GS*HNSC*ATE/GLGERPGGICGVSS SVSTQGPMP*CGQQGN*ALESCRGP ATAALSEQSPASPSSRAARA
4462	9959	A	4758	76	194	
4463	9960	A	4759	310	551	SSKQSSAKPPFCLPNPGKVCRSGRS RT*GCNLQKGSGPEKGRRFGHPPE WTIFPSVQRQGQA*FDSDSPPTNGIP GEWKG
4464	9961	A	4760	1	1165	LRWQREEGQKAGVHVGTMTQHLR PQPGAAVLPAALAPPPKHQFSLQAS SPSRLGRAGLAGGPSRAGLLC*WRR LSFLPSSFPPSPRSWGARSRRRARGQ VGPREPAGRSAGDRGVGGRFGGPL ALSFFATGLLRASCAPAFQEVTVLG KAVQWRLEPGEPFTEG*ALAGTLG LGKH*QGRQGK*GWG*PSLANARQ LGKPLQVLGWLGHVEGRPGRAVK VTGVRSWSCLPGSTGVGDRSRATQ LPAGP*VSLRVDQGEAVTGWGGRA GARGSPGRQ\GEPRHSARG*GPESLP LPVTRNSLVGGLSESN*ACPCR*QK ERLSIRGVPERRPFSGPEPGRGPASC SGLPTTGGTEERRKEGKRAAAISKA ALPGWARLPDQPGPAATGSK
4465	9962	A	4761	1	389	EETLPLFADDMILYIIKKKQKTKKTT KESTKRY*N**M\NVFGKVAGYKV NTQKSIN*QYTI*KVKLAS\FSSSPQK NKIGINLTKEIQNVYSENYKTLKEIK DLNK*ESIPCSQIRRFNIVKMTVLLK LI
4466	9963	A	4762	1	346	RACL*FQLLGRLRQGDGLSLGIRGC SGPGWHHHSPAWATEKDPVSKTNK QNIKH/LRKSPLSRDEKILREKREEE KILAYHYLEKSAIYSISFFFLTKHILN

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						TPVCWFSSEHIIYF
4467	9964	A	4763	2	468	FPSLPSFFSRFLFCIITVM\F*VLDPLS LSYLTLILIPHLKIEFNFEK/CVNH/CF LLMLLLLFLLL\CTY*MCLGPFYFLP CLSFSSVFHFLSLCCIIGNLFRYIFKFI NFELC\CYVLYT*DLFYF*KFSLVIF* IY*FFLSIMLSL*VFFHLKHFIF
4468	9965	A	4764	3	364	RNLKLISEYCKISG*KVNIENQ\VFL YISNGQVEFEIKNTIPL*AHT*KMKY LDINVTKYVQDPYEENYKILMKKIK EQME/NIPCL*I/GRLNTKTSVLPNLE **ITAIPIKIPASYFVDTN
4469	9966	A	4765	1	755	EESILEE\VLEALTSAGEEKKIDRFFC IVEGLRHNSVQLQVACMQLNNGLG TSSGELEFKLHIKNEFMPCGLKEILP NLKCLKNDGLDIQLKGFDEHKKED LVELSHRLEDIRAELDEAYVVYNM VWSTV*ETRAEGYFISILQHLLLIRN DYFIRQQYFKLIDECVSHIVLHRDG MDPDFTYRKRLNLDLTQFVDI\CVD QAK\LKEFEEKALELYKKFEKEFT\D PQENSR*NCAKKEAQIYGPFNPNSK TF
4470	9967	A	4766	12	321	KSCDWAERLVTLV/WN/PYFKNLSN SYYKQLSPMGGYLNSWAHTLTEWI IDNILDQLIFPKLQKEVG*ESWETVV ITNHRDLFSLWLHYLSAVKTPGINGI CQHNY
4471	9968	A	4767	2	375	MSSPLPSPWSPCLLPGQAPGPTLPVP PAETLSVSPACFLRLPINPSPSQ*APA WRQLTADWGGHSALGLPGCPGPSI\ TWPSHSASHLLPQRNQGPPMLGYA HLPGHLPTNVLPSGHTPALERPK
4472	9969	A	4768	3	338	QSLALSPRLECSGAILAHCHFC/LPG FT*FFCLSLPSSWDYRSPPPT/RQLIF VFLVEMGFHHLGQAGLELLTL*SA HLGLPKCWDYRHEPPRPAQRPKLK NLK*LTTVARFTI
4473	9970	A	4769	66	365	LRDEQQHGGPWTSPLSRPPTGKRA RGRSACPQLTH*PGTAARKGASPGR SRALALPTRCPGPACGGREPRLQAR GVP/R*IPPRRGPHGAPSGLPPGPVG C
4474	9971	A	4770	3	345	KRGTPLAGEMAEGHCL\CLPLGTEY LTV\NPIVHLFNSEIG*K\RPVA\KVR HVYSITASIFFTPLRCLCGEKHISGLR ARSGIVLSLELNHGIDSFAHM*SCDL ILII\TLLSYYI
4475	9972	A	4771	2	352	KRGKPLAGEMEEGHCL\CLPLGTEY LSVKP\IVHLFNSEIGEK\RPVAGG\R HVYSNTASLFFTPLRCLGGEKHKSG LRARPGIVLSLELNHGIDSFAHM*FV DLLLIITLLSYYIPFR
4476	9973	A	4772	1	296	QRSVKISISENGNSHMEIVSFSLIFCQ FLLHVFCSIHIYDCYIFLLI*YPINRQ CLFAY*YSDIKFYSDIN/ISYFLCLLC MSFYPLSTCIYMGLVFIF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4477	9974	A	4773	2	859	GRWPTQPTSLQGGQTLGDVREAFS RRP*NGERQGAPPACPLPRSLGLWR P\WGPLSVTT*NRSWSCYCWLRLV/ GWKGSRAVVKALGSPEAAWHLLG PDAALQPCHFSQPQRRCRGRPPFLP LSGWAGPWECWPTCQAGRT*IPEG GGGSC*GPQVNDLQRHTEENVLRC DLPHPALAAWGTVSPG/SHPAPQ*T EV*RSAQSSFRPQCPLTSPARGTPGS SRRLLCGVPP/CGPLLMLCPLPVPEV GLGPFLRELLNTKKLNCFVNKQKV PNKPACHLGDGPSLPHQIC
4478	9975	A	4774	158	517	RCRSGYVDQVAGLFCFVLRQSLTF VTQAGVQWHDLSSLQPLPPRFN*FS CIILLSSWDYRCMPPCLANFGIFLR/E RGFTMLGMLVLNC*PQ/CDPPTSAS QSAGITGMGPPHLGLSCSIKK
4479	9976	A	4775	1	165	GSLLPLLFNIILEVLAKAIRQEKSIQN EKEKV*LSLLTDHMI/YM*NPTVKK LTT*KLTT
4480	9977	A	4776	2	516	QNPCISERQYCCEKLPLERSSRPQDS AGQPVT/HAHCSLSSTVDLCPPLLAT HRISCWH*QDEVQGGRD\SVDKGD LVALSLPAGHGDTDGPISLDVPDGA PDPQRTKAAIDHLHQKILKITEQIKI EQEARDDNVAEYLKLANNADKQQ VSRIKQVVQKKNPEAAQTIGQLD
4481	9978	A	4777	154	406	CTDIQGYPGSRSVAQAGVQWHNL\ CLSLPSSWDYRRPLPRPANFLYF*ER RGFTVLARMVSIS*PCDPPASASQG AGITGVSHRT
4482	9979	A	4778	1	429	ARLETNSRSVAHGGVQCHDLSSQQ PPPPGFKGFSGLSLPSSWDYRRPPPC PR*F*YFY*RRGFTVLARMVSIS*PC DPPALASQSAGITGLSHCAR/LERES HSIA\RAGGQWFHLGSLQPPPPRFK* FSCLSLPSSWDHRCPVD
4483	9980	A	4779	1381	1787	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
4484	9981	A	4780	1147	1553	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
4485	9982	A	4781	1456	1862	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
4486	9983	A	4782	889	1295	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D

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						SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
4487	9984	A	4783	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
4488	9985	A	4784	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFFCS/RD TVSLCYPGWSRVA*SRITATSA\PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCLSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFIYLFIYFHRDEGSLCCPGWS* TPELK
4489	9986	A	4785	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
4490	9987	A	4786	3	305	FFFLRKSL/GSV/TQAGVQWRGLRSL QPPPPRFKRFSCLSLLSSWDYRCVPP RPA/NFLYF**RWGFTTLARMVSIS* PCDPPASASQSAGITGISHRAQPIKY
4491	9988	A	4787	1172	1688	VFFGVFVFVFVFVFFPKLTSGTIPWA SPEVMIYPPTHS*VCEAPSFPYVFSH LFS\LQSPSHLVCLFLCSF*DGVSLCR QAGVQWRSLGSLQPLTPWFKRFSC LSLPSGWHH/RRPANFCIF/M*RRGF TMLPRMVSISSPRDPPASASQSAGIT GMSHRARPQSSVFKQSFLSR
4492	9989	A	4788	641	1074	VLNLVEFVTRELAFSTNVFFCFFFVF FCFFLRRSL/DSVTQAGVHWLDLGS LQAPPPRFTPFSCLSLPSSWDYRRPP RRPANFLYF**RRGFTRLARMVSIS* PCDPPASASQSAGITGVSHRARPTN VNKAITNGLFTYFFFNEE
4493	9990	A	4789	7273	7925	IVSLFLFILLVFWWWCFFFFFFFETE SCSVAVAQAGVQWHNLGSL\QAPP PGFTH/LFSCLSLPSSW\DYRRPPPRP VNFFFFFHF**RRGFTML\ARMV\LIS *PQVICPASASQSAGITG\LSHRVRQ GPHNLLTNQVNKFFFFFLETESHS\V TQAGVQ*HDLGSLQSPPPGLKRFSC LSLLSS*DYRLLPPHPTHF/CVFLVE NGNSPCWPGWS*TPDLR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4494	9991	A	4790	156	391	IPHSYIRKFYSFKMAILSP/KLIYSINA ISKKIK*AFLKKTDELILTFI*KGKES VLDKPILKKKNNIVGLKICDFETYY
4495	9992	A	4791	365	506	GRHHACLIVDRALVFPS/CQVGRAA HFLPLPGPCPAWTPPSRSLRPGP
4496	9993	A	4792	2	503	LTHPAGARPVLLTTPESFEGPCFGTP HGQSLSQSAFSRGHSLGDTVGVTG QVGS/LLSGGGVRAG/GAGGGGGA GFGSRLALKAAGERGEKPREPVPPP *QR\GPHTKAPWT*AGQGQPPGRAC SPG/PPAEPASQPLTPGPGRRLPGGK RSRRDRARGAARKMGLLFPLD
4497	9994	A	4793	3	389	FQDLIKR*KATIIKTLWY*HKNRY/D IDQQNRIEN/SKHRLSHLIFDKGTRTI Q/YGREQLSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSP IPDIGFHNDFLNMTPKAQATTKK
4498	9995	A	4794	27	285	VFFFFFFFLRRSLALLPRLECSGTIVF LVETGF\TMLARMVSIS*PRDLPALA SQSAGITGVSHRARPASFNFLTINILP PLLLWTF
4499	9996	A	4795	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSLRTFSSHSLNMELVQD LTASAPMYSSTSRDPP/CLGLPKCW DYKREPPRPAH
4500	9997	A	4796	74	463	HISQHDRSYLQVLLASYKTASFLFFF LRQSL/DSVTQAGVQWRDLGSLQA PPPGFTPFSCPQSPK*L/SSWDYRRPP PRPANFFCIFIVEKECFTLLARMVSIS WPRDLPASASQSAGITGMSHRARP AQVS
4501	9998	A	4797	1	337	KKLISGFNVIPIKTPANPCVKIDKLIL KFIWHCKARRIGKAMWNKIKYGGL IQ*DLKICHKVRIIEIVWY*LQGRQ/I DQ/WEQ/IQSPEIDPNIYSHLTYDKSP TAIQRRKIYPF
4502	9999	A	4798	3	331	KNYKTLLREI/KEELN*WKDIPRLW LRRLNIVKMSFL/SKFIYRLDSIPIK/ MPSRHLFL*KLILKQILKFIWEGKGP GIAKTILKKNKFGGFTLLNFNTYNK AANSRVLVLG
4503	10000	A	4799	3	340	INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKLVWKFKAHGIGKT TLKKNRVP\IPKFSSSSSSSSSSYWNE DRNINQWN*IDNLKINPCVCGQLIF NKDAKTNEER
4504	10001	A	4800	46	195	SPATLGRPEVGPDS*GPGDRDHAGL TMVKPPVFYLKNYWIMRSGDRDHP G
4505	10002	C	4801	353	442	MPLLYVQRLFARTGLCATLFGRMM SPLYV*
4506	10003	A	4802	1	273	FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGLCKHNEKSP LSVQGRIYVLRNQKG
4507	10004	A	4803	57	231	

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4508	10005	A	4804	2	169	
4509	10006	A	4805	698	1231	
4510	10007	A	4806	58	2674	
4511	10008	A	4807	7	235	
4512	10009	A	4808	1	245	FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGFHLVSQDGL DLLTS
4513	10010	A	4809	175	394	NFLRYSHFKKCNRRPGAVVTPVIPA LWEAEAGGS/CRSGDRDHPG*QGE GKRGSFLKFQEVSGAPNKFSWILPL
4514	10011	A	4810	65	2712	SGSGHCLAEAASMGPWGWKLRWT VALLLAAAGTAVGDRCERNEFQCQ DGKCISYKWVCDGSAECQDGSDES QETCLSVTCKSGDFSCGGRVNRCIP QFWRCDGQVDCDNGSDEQGCPPKT CSQDEFRCHDGKCISRQFVCDSDRD CLDGSNEASCPVLTCGPASFQCNSS TCIPQLWACDNDPDCEDGSDEWPQ RCRGLYVFQGDSSPCSAFEFHCLSG ECIHSSWRCDGGPDCKDKSDEENC AVATCRPDEFQCSDGNCIHGSRQCD REYDCKDMSDEVGCVNETLCEGPN KFKCHSGECITLDKVCNMARDCRD WSDEPIKECGTNECLDNNGGCSHV CNDLKIGYECLCPDGFQLVAQRRCE DIDECQDPDTCSQLCVNLEGGYKC QCEEGFQLDPHTKACKAVGSIAYLF FTNRHEV\RRMTRTRSGYTSFIPNLR NVVALNTEGPSNRIYWSDLSQRMIC STQLDRAHGVSSYDTVISRDIQAPD GLAVDWIHSNIYWTDSVLGTVSVA DTKGVKRKTLFRENGSKPRAIVVDP VHGKHRPCT/WPGVLCTCQVTSAT* DVRATIRR*ML/WFPQRTLEKAHLV SGREKQEESIIRCLRVKVWLTYEMQ \DLGGG*TRL*ITQAKMNAENWL*L EEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRG VNWCERTTLSNGGCQYLCLPAPQI NPHSPKFTCACPDGMLLARDMRSC LTEAEAAVATQETSTVRLKVSSTAV RTQHTTTRPVPDTSRLPGATPGLTT VEIVTMSHQALGDVAGRGNEKKPS SVRALSIVLPIVLLVFLCLGVFLLWK NWRLKNINSINFDNPVYQKTTEDEV HICHNQDGYSYPSRQMVSLEDDVA
4515	10012	A	4811	49	361	STSYPITGSHAFL*PQNVVDAETNS* HINNVNLRLKIIKLLEENTEKNCHD LGLSTDYY/SVTPKA*ATTTKI\DKL ELIKIKNFCTSKDITYKVKRLLIGNNI CK
4516	10013	A	4812	2	346	EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4517	10014	A	4813	2	356	EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCKSFM
4518	10015	A	4814	1	357	VRPHHTNKKRVRLR/VRVNIKVRD KVSTEVKDKIKNQAAVIVKLGVQIK AGPWVRVKDWVRLEVKIKNRDQV RGEAEVRRIGQQLRTKTRPKLNVHP KRNGSIN*NIHTVECYSTIKKQ
4519	10016	A	4815	1	323	PVRGTEQSNKSWASGLQPGWGRAE QLAWGSFNLSKWPSGGGDPQPILLS RVQNMGRLAR*EAPCQPQPQLPSR RSSPVPHQHL\PPCHPCGASLSPALA WPPPPPSRS
4520	10017	A	4816	1908	2324	ILASSLRANPGFIRNFHLFFFFFYFLR RSL/DSVAQAGVQWHDLGSLQAPPP GFTPFSCLSLPNSWDYRRPP/RHHAR LISFFLFLVEMGF\TMLARMVSIF*P WDLATSASQNAGITGVSHHTHPRP VIKYLPSSSPNLAG
4521	10018	A	4817	1	273	RPRRRYPHSWWFL\QEVAIFTLIEKV VFYYSHRLFLHPAFYKKIRKIHHKW TAPIGVISL*AHPIEHAVSNMLPVDP VNLRQSIRTVLFHQ
4522	10019	A	4818	3	293	DHVSPGVQDQAGQYSKTP\SLQKQ KQKTNRHGSAYLWSELLGSLRQED HLNPGVRGCSELLLGHCSPAWAAK *DPVC*KNKTKNLIAGGHPRSFWIQ
4523	10020	A	4819	2	170	KLGFIKIKDFSSVKDNVKGMRRQAT DW/DFIKIKDFSSVKDNVKGMRRQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4524	10021	A	4820	52	228	WASGHVRPYRVLNNFISNQK\MDF KEDLSGIAEMFKTPVKELLIVL*TCL IVAFKSDNS
4525	10022	A	4821	22	376	TGTVIKIAWY*HKDRHMDQ*NRINS SETNPNI*SKVQRPFHWRASSSSSSS SSSSSSSSSSSS/PSSSSSSSSSSSSSSSS SSSSSSSSFIQGNTGINLTDFGLGNVF LDMTPKAQAKE
4526	10023	A	4822	151	379	SIPGIQSWFNIQKSINVFYHIVILNTQ HRSSSSSSSSSSSSSSSSY*LMIKF/LNK LGIEGNFLILIKAIHGKPTVNH
4527	10024	A	4823	3	479	RDEVSPHCPGWSQTPGLKQSSCLGL PKC*AYRHEPLGL\ILFFH*ATQETQ ARAGWSYASHFVDERTEAQR/V*G TCPRSHANYVLEDLICVLF*DRVCS VAQAGVQWHDLSSLQPPPPGFK*FS CLSLPSSWDYRRFATTAS*ILAF*VE MGVRHFARLV
4528	10025	A	4824	1	57	GKRYTRSDELQRLRRAHTG\EKKLV CPECSQRSMRSDRLTGHIRSHQNKK GIH*SDELQRLRRAHTG
4529	10026	A	4825	3	602	VDKNHTLSLLCQPSHGDCSRFSAST CLIRSRFHFNFNTFKIF*KLGDSMLT AVSVARDCGMILPQDKVIIAEALPP

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						KDGKVAKINWHYADSLTQCSHPSA IDPEAIPVRL/CP**LRGSSNDSLSFC NEWEIILSDTGGIFK/HLVPKGSNLG VCVCSHECIATVF*KNLYYCFQLML HGTVFARMAPDQKTQLIEALQNVE
4530	10027	A	4826	3	241	TSFSCLSLLSSWDYRCPPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4531	10028	A	4827	3	241	TSFSCLSLLSSWDYRCPPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4532	10029	A	4828	2	321	KAVLRRKFIATNT*\KK*TSQIKNLL KKLQEKNKFKPKVSRRKTIQRSEQK *IQTRKPGEKINKTKGSSSSSSSSSSS SSSSSSQREDLNQIGNEREDITTGTT EIQ
4533	10030	A	4829	132	290	LVTSE***IYQIFFFSPEMESHSVSQA GVRWSNL\SSLHPLPPGFKRFSCFSL
4534	10031	A	4830	645	1201	GGRDLLRTHSVGPSTPQTIPVLTPPG *CACKTQDVPSPHS/PPMKELWPGA PQGSPGRLSPQPPH*RPSPHSPCTLW PAL/PGLASTEGWGAIALYILEKNW GREGLNLPPA*PFCPPQPSPHGSLVF PSKCASREAPTSNPCLQPQIPRLPSR PKAQPAPTHLGGAAHTRISAGVAR VCAGAFGGQA
4535	10032	A	4832	115	454	TMMTSWINCFRKG*DDVEHHALHI NLRGKKFILFLPIQEGLTRGRKQ*AN TVGHFQLGFRLYKISGLEKLKLSKL STQWLLKP\LHPDQL*TRAELLG*ES LDKYDQDPEALIR
4536	10033	A	4833	1	638	ERQSVPGFKASQDRLTLLVRAYTN Q*LKLRPLLIF\HFENPRALKNCAYS TLSVLCQWNNKAWMSAH\LFTGW LTKYFKLTIETYCSE\KTTPFKILLFI DNLAGHPRALMEM*KEMNVFMPA KTTSIMLPLI\SSFNSYYLRNRIHRTF VVVAQSWLQCPTTAISDIQIGPVAM GLLLIPSAFVLCWLSIQQVSKLKHF HSHHSYFLRFWRLTA
4537	10034	A	4834	2	6053	KEILQEYLEISSLVQDEVVAIHREM AAAAARIQPEAEYQGFLRQYGSAP DVPPCVTFDESLLEEGEPLEPGELQL NELTVESVQHTVQLLGKRQVLQEA LQGLQVALCSQAKLQAQQELLQTK LEHLGPGEPPPVLLLQDDRHSTSSSE QEREGGRTPTEILKSHISGIFRPKFS LPPPLQLIPEVQKPLHEQLWYHGAIP RAEVAELLVHSGDFLVRESQGKQE YVLSVLWDGLPRHFIIQSLDGSRPL RMEAADPGSPALQNLYRLEGEGFPS IPLLIDHLLSTQQPLTKKSGVVLHRA VPKDKWVLNHEDLVLGEQIGRVPQ RGSNSQRAWVRGPNTGAPHPGVGS RMGRKRRRELRDWEGRGRSPRPFQ GNFGEVFSGRLRADNTLVAVKSCR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ETLPPDLKAKFLQEARILKQYSHPNI VRLIGVCTQKQPIYIVMELVQGGDF LTFLRTEGARLRVKTLLQMVGDAA AGMEYLESKCCIHRDLAARNCLVT EKNVLKISDFGMSREEADGVYAAS GGLRQVPVKWTAPEALNYGRYSSE SDVWSFGILLWETFSLGASPYPNLS NQQTREFVEKGGRLPCPELCPDAVF RLMEQCWAYEPGQRPSFSTIYQELQ SIRKRHRPRCSSSAAPAHMLTALHS PGLLPPASTLPAGCSAVSSLCPCCCQ GFLFRAETIKPLVPTEHSWHVHSSG RQVSEGTSAGNIEQARKGKGLEEC AVPTGGSTPLPEGRNDRDLRLPGPE PASEAGGPARGRRTERSGCPGAQL GPRQRPPEQGATGERAPAFACVAA CTRAAVPGRVCVEASMKLKKQVT VCGAAIFCVAVFSLYLMLDRVQHD PTRHQNGGNFPRSQISVLQNRIEQLE QLLEENHEIISHIKDSVLELTANAEG PPAMLPYYTVNGSWVVPPEPRPSFF SISPQDCQFALGGRGQKPELQMLTV SEELPFDNVDGGVWRQGFDISYDP HDWDAEDLQVFVVPHSHNDPGWI KTFDKYYTEQTQHILNSMVSKLQE DPRRRFLWAEVSFFAKWLVGNGQL EIATGGWVMPDEANSHYFALIDQLI EGHQWLERNLGATPRSGWAVDPFG YSSTMPYLLRRANLTSMLIQRVHY AIKKHFAATHSLEFMWRQTWDSDS STDIFCHMMPFYSYDVPHTCGPDPK ICCQFDFKRLPGGRINCPWKVPPRAI TEANVAERAALLLDQYRKKSQLFR SNVLLVPLGDDFRYDKPQEWDAQF FNYQRLFDFFNSRPNLHVQAQFGTL SDYFDALYKRTGVEPGARPPGFPVL SGDFFSYADREDHYWTGYYTSRPF YKSLDRVLEAHLRGAEVLYSLAAA HARRSGLAGRYPLSDFTLLTEARRT LGLFQHHDAITGTAKEAVVVDYGV RLLRSLVNLKQVIIHAAHYLVLGDK ETYHFDPEAPFLQVVGWEEAEPMM VLPFRLTEFQDDTRLSHDALPERTVI QLDSSPRFVVLFNPLEQERFSMVFL LVNSPRVRVLSEEGQPLAVQISAHW SSATEAVPDVYQVSVPVRLPALGLG VLQLQLGLDGHRTLPSSVRIYLHGR QLSVSRHEAFPLRVIDSGTSDFALSN RYMQVWFSGLTGLLKSIRRVDEEH EQQVDMQVLVYGTRTSKDKSGAY LFLPDGEA\SPTSPRSPPCCVSLKALS SQRWFRTMSTFTRRSGFTICQGWR GCLWTYHPWWTSGTTSTRSWPCTS IQTSTAR/VIFFTDLNGFQVQPRRYL KKLPLQANFYPMPVMAYIQDAQKR LTLHTAQALGVSSLKDGQLEVILDR RLMQDDNRGLGQGLKDNKRTCNR FRLLLERRTVGSEPDFFSKLAAMFR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GLIFHSSRSGNREVQDSHSTSYPSLL SHLTSMYLNAPALALPVARMQLPG PGLRSFHPLASSLPCDFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFDC GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4538	10035	A	4835	1	6606	MGFSSELCSPQGHGVLQQMQEAEL RLLEGMRKWMAQRVKSDREYAGL LHHMSLQDSGGQSRAISPDSPISQS WAEITIQTEGLSRLLRQHAEDLNSG PLSKLSLLIRERQQLRKTYSEQWQQ LQQELTKTHSQDIEKLKSQYRALAR DSAQAKRKYQEASKDKDRDKAKD KYVRSLWKLFAHHNRYVLGVRAA QLHHQHHHQLLLPGLLRSLQDLHE EMACILKEILQEYLEISSLVQDEVVA IHREMAAAAARIQPEAEYQGFLRQ YGSAPDVPPCVTFDESLLEEGEPLEP GELQLNELTVESVQHTLTSVTDELA VATEMVFRRQEMVTQLQQELRNEE ENTHPRERVQLLGKRQVLQEALQG LQVALCSQAKLQAQQELLQTKLEH LGPGEPPPVLLLQDDRHSTSSSEQER EGGRTPTLEILKSHISGIFRPKFSLPP PLQLIPEVQKPLHEQLWYHGAIPRA EVAELLVHSGDFLVRESQGKQEYV LSVLWDGLPRHFIIQSLDGSRPLRM EAADPGSPALQNLYRLEGEGFPSIPL LIDHLLSTQQPLTKKSGVVLHRAVP KDKWVLNHEDLVLGEQIGRVPQRG SNSQRAWVRGPNTGAPHPGVGSRM GRKRRRELRDWEGRGRSPRPFQGN FGEVFSGRLRADNTLVAVKSCRETL PPDLKAKFLQEARILKQYSHPNIVR LIGVCTQKQPIYIVMELVQGGDFLT FLRTEGARLRVKTLLQMVGDAAAG MEYLESKCCIHRDLAARNCLVTEK NVLKISDFGMSREEADGVYAASGG LRQVPVKWTAPEALNYGRYSSESD VWSFGILLWETFSLGASPYPNLSNQ QTREFVEKGGRLPCPELCPDAVFRL MEQCWAYEPGQRPSFSTIYQELQSI RKRHRKHRAGTERKGTRGMRCTD RRQHPFARGAQRQRPKATWAGAG FRGWRTRAEPAQRSAPAARGPAGE LQQRAEQGATGGRAPAFACVAACT RAAVPGRVCVEASMKLKKQVTVC GAAIFCVAVFSLYLMLDRVQHDPT RHQNGGNFPRSQISVLQNRIEQLEQ LLEENHEIISHIKDSVLELTANAEGP PAMLPYYTVNGSWVVPPEPRPSFFS ISPQDCQFALGGRGQKPELQMLTVS EELPFDNVDGGVWRQGFDISYDPH DWDAEDLQVFVVPHSHNDPGWIKT FDKYYTEQTQHILNSMVSKLQEDPR RRFLWAEVSFFAKWLVGNGQLEIA

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						TGGWVMPDEANSHYFALIDQLIEG HQWLERNLGATPRSGWAVDPFGYS STMPYLLRRANLTSMLIQRVHYAIK KHFAATHSLEFMWRQTWDSDSSTD IFCHMMPFYSYDVPHTCGPDPKICC QFDFKRLPGGRINCPWKVPPRAITE ANVAERAALLLDQYRKKSRLFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLFDFFNSRPNLHVQAQFGTLSD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYYTSRPFYK SLDRVLEAHLRGAEVLYSLAAAHA RRSGLAGRYPLSDFTLLTEARRTLG LFQHHDAITGTAKEAVVVDYGVRL LRSLVNLKQVIIHAAHYLVLGDKET YHFDPEAPFLQVVGWEEAEPMMVL PFRLTEFQDDTRLSHDALPERTVIQL DSSPRFVVLFNPLEQERFSMVFLLV NSPRVRVLSEEGQPLAVQISAHWSS ATEAVPDVYQVSVPVRLPALGLGV LQLQLGLDGHRTLPSSVRIYLHGRQ LSVSRHEAFPLRVIDSGTSDFALSNR YMQVWFSGLTGLLKSIRRVDEEHE QQVDMQVLVYGTRTSKDKSGAYL FLPDGEA\SPTSPRSPPCCVSLKALSS QRWLRTMSTFTRRSGFTICQGWRG CLWTYHPWWTSGTTSTRSWPCTSI QTSTAR/VIFFTDLNGFQVQPRRYLK KLPLQANFYPMPVMAYIQDAQKRL TLHTAQALGVSSLKDGQLEVILDRR LMQDDNRGLGQGLKDNKRTCNRF RLLLERRTVGSEPDFFSKLAAMFRG LIFHSSRSGNREVQDSHSTSYPSLLS HLTSMYLNAPALALPVARMQLPGP GLRSFHPLASSLPCDFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFDC GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4539	10036	B	4836	114	255	VQPRRYLKKLPLQANFYPMPVMAY IQDAQKRLTLHTAQALGVSSLKDX*
4540	10037	A	4837	1	452	LDGRQLSV/SRHEG/FP/LRCIDS/GTS ELALS/N/RYMQVWFSGL/TGLLKSI RRVDERHEQQVHMQVLVYGTRTS KDKSGAYLFMPDGEAKP\TSPRSPP CCVSLKALSSQRWLRTMSTFTRRSG FTICQGWRGCLWTYHPWWTSGTTS TRSLHFSFN
4541	10038	A	4838	3	3543	QLGRLGPERRGGRALTVCVEASMK LKKQVTVCGAAIFCVAVFSLYLML DRVQHDPTRHQNGGNFPRSQISVLQ NRIEQLEQLLEENHEIISHIKDSVLEL TANAEGPPAMLPYYTVNGSWVVPP EPRPSFFSISPQDCQFALGGRGQKPE LQMLTVSEELPFDNVDGGVWRQGF DISYDPHDWDAEDLQVFVVPHSHN DPGWIKTFDKYYTEQTQHILNSMVS

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						KLQEDPRRRFLWAEVSFFAKWWD NINVQKRAAVRRLVGNGQLEIATG GWVMPDEANSHYFALIDQLIEGHQ WLERNLGATPRSGWAVDPFGYSST MPYLLRRANLTSMLIQRVHYAIKK .HFAATHSLEFMWRQTWDSDSSTDI FCHMMPFYSYDVPHTCGPDPKICC QFDFKRLPGGRINCPWKVPPRAITE ANVAERAALLLDQYRKKSQLFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLFDFFNSRPNLHVQAQFGTLSD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYYTSRPFYK SLDRVLEAHLRGAEVLYSLAAAHA RRSGLAGRYPLSDFTLLTEARRTLG LFQHHDAITGTAKEAVVVDYGVRL LRSLVNLKQVIIHAAHYLVLGDKET YHFDPEAPFLQVDDTRLSHDALPER TVIQLDSSPRFVVLFNPLEQERFSMV SLLVNSPRVRVLSEEGQPLAVQISA HWSSATEAVPDVYQVSVPVRLPAL GLGVLQLQLGLDGHRTLPSSVRIYL HGRQLSVSRHEAFPLRVIDSGTSDF ALSNRYMQVWFSGLTGLLKGSGLC FLA\SIRRVDEEHEQQVDMQVLVYG TRTSKDKSGAYLFLPDGEA\SPTSPR SPPSCVSLKALSSQRWLRTMSTFTR RSGFTICQGWRGCLWTYHPWWTS GTTSTRSWPCTSIQTSTAR/VIFFTDL NGFQVQPRRYLKKLPLQANFYPMP VMAYIQDAQKRLTLHTAQALGVSS LKDGQLEVILDRRLMQDDNRGLGQ GLKDNKRTCNRFRLLLERRTVGSE VQDSHSTSYPSLLSHLTSMYLNAPA LALPVARMQLPGPGLRSFHPLASSL PCDFHLLNLRTLQAEEDTLPSAETA LILHRKGFDCGLEAKNLGFNCTTSQ GKVALGSLFHGLDVVFLQPTSLTLL YPLASPSNSTDVYLEPMEIATFRLRL G
4542	10039	A	4839	2	438	FVPAKVAGAAEPDEDGGRSRLRDC GDYTPSERLGPKGAMLWFQGAIPA AIATAKRSGAVFVVFVASDDEQSTQ MAASWEDDKVTEASSNSFVAIKIDT K/QMHLLKSETSVANGSQSESSVST PSASFEPNNTCENSQSRNAELCEI
4543	10040	A	4840	1	1608	
4544	10041	A	4841	1	3117	MAPEWRPGTTASLPSGPGARSVCSL RSPEAGSASVFVRLCGPRNLGWFGP HLRLRTSAHARQRHPKTRASAREN TSRHSRNPSVSVPQDLLSLASRCAG SIPITLESCLPVGLSKDVWPLTIEPKV KVFIFNLKLPDCPSTMKNPASLLFSL FEGEWAIAEEVLSDIWCTGVLAINK DQVLTIGFDINEFLSCSSSSKKSMSC SLTGSLALQPDQQQDHETTDSSPAS AYQRIWEAFANQSRAERDAFLQDT FPEGFLWGASTGAFNVEGGWAVG

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						GRGVQPKHVKEAFRLLNKSIIRVET PDVNLDQEEEIQMEVDEGAGGING HADSPAPVNGINGYNEDINQESAPK ASLRLGFSEYCRISNLIVLHLRKVEE EEDESALKRSELVNWYLKEIESEIDS EEELINKKRIIEKVIHRLTHYVEYFSS LHASQITHYKVFLSWAQLLPAGSTQ NPDEKTVQCYRRLLKALKTARLQP MVILHHQTLPASTLRRTEAFADLFA DYATFAFHSFGDLVGIWFTFSDLEE VIKELPHQESRASQLQTLSDAHRKA YEIYHESYAFQGWLAFTHMSQTLA NKIRVRGMAQESCSHGSSVGYLQH PGSEQVQFPRTTSPCSSQQLQGHQC TAGPPPPPGGGMVMMQLSVPNNPQ SCAHSPPQWKQNKYYCDHQRGQK CVEFSSVDNIVQTSLNCTDPVVCVP SSFF\IGDSGIPLEVIAGSVSADELVT RIHKVRQMHLLKSETSVANGSQSES SVSTPSASFEPNNTCENSQSRNAEL\ CEIPPTSDTKSDTATGGESAGHATFL FREPSGCSDQRPAEDLNIRVERLTK K\LEERREEKRKEEEQREIKKEIERR KTGKEMLDYKRKQEEELTKRMLEE RNREKAEDRAARERIKQQIALDRAE RAARFAKTKEEVEAAKAAALLAKQ AEMEVKRESYARERSTVARIQFRLP DGSSFTNQFPSDAPLEEARQFAAQT SVRVTSSEPPNPASSSKSEKREPVRK RVLEKRGDDFKKEGKIYRLRTQDD GEDENNTWNGNSTQQM
4545	10042	A	4842	3	790	GARGTPFLSPASVESSVLLCLLVPHP VLSRGPPASPPSSYHPSLGPGG/GGQ *PLPEYGLESSEQN*GLSPGEDPGNP GGPFWGSG\PAGSLMEA*GNKRDA PPPPG\DPSCSAPC/GDPPGMQGIQDS LPCHTASQKGGAFPFGPMAPGRVL HQQGPL*GPSRLSQESPSAGPPMPQ LPSWVLCQVRPRAWGCWEPKGPPG TQFPPRFPDPSGTPCPPGYLEIFLLDP IPPRNWLAPLAAAAQ**/PWGRWE MPMALPRGGLPLYT
4546	10043	A	4843	1	1026	
4547	10044	A	4844	1	722	MALEQRLKGGSGAALRSKAFPAEG TAGAKALGQESDWSIGGAVSKPVF VQSVRELVADPCASNPCHHGNCSSS SSSSSDGYLCICNEGYEGPNCEQAL PSLPATGWTE/CHGTPTASACSCYS GA*Q/QSCLALRQR*HCLPGSRKQG\ KSCRNEMGSSGGDPRYCLWECQF* QLCGWPPGIL*SATEHLSQDSARCH CLTDFALEGHGHRIPTVLPHRWTKC DPPSGFRGTGPPGGDARLGE
4548	10045	A	4845	2	2028	CSPAAPRRPVRSCCPRWPCCCCCSE RGPEAAPWPTRCPPRPCL/LPGPCAA QPCRNGGVCTSRPEPDPQHPAPAGE PGYSCTCPAGISGANCQLVADPCAS NPCHHGNCSSSSSSSSSDGYLCICNEG

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						YEGPNCEQALPSLPATGWT/AIHGT PTASACSCYSGA*QNPASLSGNGDT AYLAAENRAESCRNEMGSSGGDPR YCLWECQF*QLCGWPPGIL*SATEH LSQDSARCHCLTDFALEGHGHRIPT VLPHRWTKCDPPSGFRGTGPPGGD ARLGE*SLY\CFVNDSVTKS/NCGFA LNSGGE\VSTCVPGESHANDLECSG KGKCTTKPSEATFSCTCEEQYVGTF CEEYDACQRKPCQNNASCIDANEK QDGSNFTCVCLPGY\NGELCQSKID YCILDPCRNGATCISSLSGFTCQCPE GYFGSACEEKVDPCASSP\CQNNGT CYVDGVHFTCNCSPGFTGPTCAQLI DFCALSPCAHGTCRSVGTSYKCLCD PGYHGLYCEEEYNECLSAPCLNAA TCRDLVNGYECVCLAEYKGTHCEL YKDPCA\KSACLNGATCDSDGLNG TCICAPGFTG*ECDIDINEC/ATVTP CHHGG\SCLGDQPNGY\TCHCPHGW VGANCEIHLHWEVPGTWAESLTNM PRHFPLTFIHWEPFLRGPFHPYADHP DRGDLPHQPH
4549	10046	A	4846	1	703	TISCPAVRSRRPRRISCLSCPGGGGA ASGLQRAAGGTGLSWVPAGLRVCC SQRSWRPAKEEQPVQTPRRTGKGG EISDMEKPYNKNEGNLENEGKPEDE V*PDDEGKSY*EEKPYA*GNTECEG KLKADGEPGDEGQLEDNGSQEKQG KSECEGKPQGEGKPASQAKPESQPR AAEKRPA*RLCGPGKAKK/NKPDQ GDRTIFPQGLSGGLTGKASEQ*GDD ERMWRCVKGSRGA
4550	10047	A	4847	180	866	GAYVHGGRGLCVQSLFQGVSSSDF CPPIPTLVPTLRPRAPCLWCTQDPAR PPCQSQRRGLGPFQG\AGLKPSPGLL PNILLPESPSKRFNHGQLPVPQTVFG GGGSRGPPLLVPPSLPLFVFPFCGCF LSQPRGHRSPPSSP*EEG*STPLLSVC HSHTDLWGLSWAVPAGWTGPSALF SPQAVNRLPITRPAPTHPHSFPREAP GRW*TPLPTSYQSLLFYGKDLPVK
4551	10048	A	4848	112	679	KI*NMWCYSDTGQFNVVKLSVLL*I IYIFNKILSSFLVKTGKLSLKSVN/NK QQSRITKTSKEN\KRGGFMR*DIKTF YVFAVIKSVLYMQI*ID*WKIIESSET DLHISSHLIFDKDNKMEKSLKK\WDI VYSSHRKIINLDL*HIPYVNINMIWN IDLKIKRFF*IAT/ENIFVTFSNVGND FLKYQLKSKIKKLKMRMVVYQMV P
4552	10049	A	4849	33	394	GSVWHHPFEGALRGPIPGAAGKPG LGTPSHPGLSPHPAACAACPRLPGL CSCAPGSAPLPRLRP*/PAPCGSSDS VPRTP/GRRGLGSPGPPAPAAPKAE* LLQGGEFFSDPQPLAPEPRQLR
4553	10050	A	4850	2	269	LSGVCTVHIRGVCVWAGGNPSGTE LPGPLPPRPSASPPHPPPQG*GVALP\

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						PVLFCFLVLPPHPTPNLIYPPCTVPFS PLPAPFAFFCW
4554	10051	A	4851	1	543	LLSKWIIITPSGAGSGDPPPAASPRR KQRMKIMKTTRSQTPPGRAPAASA SSPTL*TPGRDLESRLRP*PTNLPVR TPPGTAAVCPLLHRP\PQKAPVLGP ARV*ERGE/DANATPKREGLKRA/PP NDTLDFLWLGTPSSTKIKWTRPPAV EPLLVLHPTPTLPPLPVVPIVTQRVE YQGRFF
4555	10052	A	4852	831	1301	FFVFTFKYKNTILLCVINQGPSSKNL FFFQGRDIHQFILSFVFRAGHLVPSQ ASPTSKRPKPFSLIPNPYLLS*FPLLIE KLVINFLKKKFPTTRASP*PNQSTSR SSPFSYPGRRVPPLQT\SSVPELRTPY WTGAPPLNGSSGYVSPTLPPPLMH
4556	10053	A	4853	1	1222	
4557	10054	A	4854	2	563	AHVIIYRFSMH*VITDVIPMLEVRSV YEINDVGTPEGEQ\TPPLPTPVGGSN PQPIPAQSHPSTSSSSSDGLRDNVPW LKVKNSPLKQSPGYQTELVIQLVW VGGEPPQQIASLAVNSSYGLVDFGN CNGIAMVDYLQKAVLLNLGTIELY GSNDPYRREPRSPRKSRQPSGAGLC DISEGLVPSKA
4558	10055	A	4855	648	1377	EYLHGGWEHLQKRSLSPATGGGQG QLGAEGGP/GPGGGAAPAHPLLAPN QACGVGLIDWRPRWTRGGTAAAG ARTPNLNPGAALTP/GRHSCVSVKK GSESLELSRRR/TLPVVSPPGGGGCE MLRPDPASSP\SSQTP*PVPGAEAQT LALSCPPNSCPAKEVGAAGF*APLH LLSPSVGEGGGASGSTPKVSSFPLPF GGPLHSP*Y*PGPENWEGGGDEGPL SHPARVPAAQSETECVPTESPFQ
4559	10056	A	4856	3	394	SQAPS/GVAAHTPPLS*AWTQPWNS IHMALASTRPNMPLRSGPA\CMPQL QLQELFTRSLVESELRIAPSEYPDES PIEQLEERRQLLEQPISLDVMLEPYI LRRSKLDLLYTDSDSDLQLYKEQGE GQGDR
4560	10057	A	4857	3	666	SLLPKIFIGCLRRASSGPGAGNMLGS PSPQPLVSILGIAESWSTLPQGQPPA NPEAWAGPAGAKTDKSKT*GHFTP ETLPNVPKKDPLQLGA*KPGGSKPS EE/VWSQ/SPGPWLRNSGFFPPSLNP RWGPFPSTLWERF*NCSQPFRALRN PPVPL*GVLRASNPWPPPHPHTHPA NMPPAPPRVRLRSSSTSAPPPWGCT QGPRGARAGA*AGAASS*SRGR
4561	10058	A	4858	3	361	FFFFRKWVNIFANYM*KKLILKIYQ QL*KLNHKVQ*LDL*MNKQNFHQK TTQM/AKKHLTGCTKLLICREMKK KTQ*QRNHLTPIRMATIYFLKNAN/C W**CNKNETHVGCWWKTKM*SLF
4562	10059	A	4859	3	397	DQPTDIILDEQ*LELFHLRTGIRRGC PVSSLPFN/IRAIRQEK*IKGIQLGKEI

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						KLALFADMILYLENPEDS/AQKL/LR LINNFSQVSGYKINAQKLGAFLYTN NVQAE/SQIKNPIPFTVAIKKLKYLKI HLAKE
4563	10060	A	4860	2	328	AHIDAVNEAMRLLEHGFHAPTMSW PVSGTLMVEPIETEDHA*LDRFWDA LINLLQGIADIEDGRICPRVNPLKMS PHSLTCVTSSHWDRA\YSEKGAAFP LPFVKPENK
4564	10061	A	4861	13	410	NKMRRQATDRDKMLAKDTFDK\GT LEIYNQFLKFNNKKMSIPIK*WAKN L/NSHLTREDIQVANKPMKRCSTSY FIKEMQIKAMTRSRCADIKMAKIQT TDDIKC*RTCTRSTNFPFPALHLFYQ LTFRKSISH
4565	10062	A	4862	3	293	DKGLKGFRGFPTFTSFGQPTWLGLG LDLPEPGN*GPGFGCGP/NSRVGPTL SNLGPGPERGPPGPPGLGV*ALKGK RADKKGGASFFPGF*KFPVGLP
4566	10063	A	4863	125	366	GIPGERRLEPPG/PKGPPGLSPQIKGN NGPGPQN*VFFGGFKTKVPFGAQG GS/GNPGPKPIFPPGPPKGRKYRVGP MAPPLQ
4567	10064	A	4864	79	336	HIATFNALSYVQASKRDKKFFACAP NYSYAVLCECLSSSIHLSSACSHVH C*RHDDDALLWQPHGSIRDDMR*HI ATFNALSYVQASKRDKKFFACAPN YSYAVLCEC\HRRVFIYRQPAPMST VFYNRKDCLQ/TVDRMLIHKVASLK TNDPILSIQAPK
4568	10065	A	4865	2	512	KIQIASIRNEIGH/LLTDATYIQRRLR E*CGQLQANKFDNLNGRDKFPGRH KLPKLIQKEMEAGRSGLPLSPRVLG LQA*ATVSGLTGKFYKTCKEEIIPIL TILFQKTEKGTLQ\SS*EETSTILIPNQ EGKKNFQNGCLSMDPGTGKVPLTK ILVNQIQQSVIHKDNISI
4569	10066	A	4866	466	1451	EVCGLKKARISLFFF*DGVSLCCPG WSAVAQSRLTATSASRV\K*FSCLSL LSSWDYKRPPPRPANFLHF**RQGF TMLARLVSIS/WIS*SVPPWPPKVLE L*AKAGDSLEPGSSRLQ
4570	10067	A	4867	3	379	NKSCQGPRTSFASAGWALKNPRWQ EQKEGLGKAGRPSGMNSSASSPTPG RKRELGMGSPSLSRSPP*CE\GRSDR LG*PP*GGQGGGGHGAPSTPGPGG\ GPGDFHSKPPDPSLVPRPTEARGSP GP
4571	10068	A	4868	2	1718	SEGAPPRRGAWGGPPARSHTLAPTP PLPP/GPLSLCFACLKWLGVD/HRDG AG*LGSQKAGGRGHPGMGQKGT PPAHAW*PTGWCTGKP*KLGFLCPF HIPPVSLACFLLSCAASDFSVLTWQ LWGP*EPPTEGGHSPFPSCRC/HRQE EGFLPVWQSPRQRPRMRPDSAPPST SARASKVGPGRGLPLLNFG/QRPNL TPYGPAPALALS*PPQRWEELAEGA

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						PGPQPP\ASKGPFSS*PKVLREPAVE TSSCASAPLAVFVRGVHTCIGG*AP GLSGGHPLTVSF*IGGIEGLDCLSPQ *AWGPGLGLEVCCGSHQASPPGPG VLGAPCPPPPCPPQGG/PAQPVGPS/P SHHGGERE*RGRPHSKLPLPPGVWG GC*RIHSRGPPGLSQPLFCF*PRRLS\ PAQPA*SKGGSRVLGSFCFPLLPGS* GTRASGRGHSPSLKPGPGRAGRQ\G ETRGS\GSPGE*GCWSQNWDRGPA GQPWATSRVSIVRGWRVPGVAGAG FLAVLPWAPPSEARWQEADQNPSA FGPKEWEAAFLPNLPCQGQQRGPSP PPPPGCRNGDPSQGLGAGAEYSLGP LPYT
4572	10069	A	4869	253	451	RWKAWFGREIKGNNPRCKRGGGK HGTG/EEIKGNNPRWKRGGGKHGT GGK/YKGNNPRWKRGGGKHGTGG K/YKGNNPRWKRGGGKHGTGGKL K/SNNPRW*REGGKHGSGGK/YKGN NPRCKRGGGKHGTGGKLK/SNNPR WKRAGGKHGSGGKFKEIIPDGSVK VESMER
4573	10070	A	4870	2	269	EGGLGLNRFPPPPGPPRRPAAACMS AP*PQR/HWPP/SPREEKASLNEPGG PGRGRGRGSGQLHGEGGPRGGE/R GNWPGGMEGEGGIDAPAS
4574	10071	A	4871	20	312	SVMNGTSICKCRANDETGLSPSPAG PKSRSRRLS*LWRPSAATDSGSPPT* PVPTPSPPAPTPARPGSRAPSSPGLA PTLTGPGG\PLRPPPPPAEEP
4575	10072	A	4872	299	472	KSISVATANPGKCLSCTNSTFTFTTC RILHPSDITQVTPR*/GVPGKSGASLL SSAVFS
4576	10073	A	4873	1	3454	MKHTLIPRIKNACLQMSSLAVPVNS LVCLGKILEYLDKWLVLDGILPFLQ QIPSKESAVLMGILGIYKCTFTHKLG ITKEQLTGKVLPHLIPLSIENNLNQF NSFISIIKEMLNRLESEHKTKLEQLHI MQEQQKSLDIGNQMNVSEETKVTN IGNQQIDKVFSHIGADLLTGSDSEN KEDGALNVPPAGAKPTQQRPTDMS ALNNLFGPQKPKVSMNQLSQQKPN QWLNQFVPPQVSPATGSSVMGTQM NMIGQSAFDVCSNEDLPEVELVSLL EEQLPQYRLKVDTLFLYENQDWTQ SPHQRQHASDALSPVLAEETFRYMI LGTDRVEQMTKTYNDIDMVTHLLA ERDRDLELAARIGQALLKRNHVLSE QNESLEEQLGQAFDVNQLQHELC KKDELLRIVSIASEESETDSSCSTPLR FNESFSLSQGLLQLEMLQEKLKELE EENMALRSKACHIKTETVTYEEKEQ QLVSDCVKELRETNAQMSRMTEEL SGKSDELIRYQEELSSLLSQIVDLQH KLKEHVIEKEELKLHLQASKDAQR QLTMELHELQDRNMECLGMLHESQ EEIKELRSRSGPTAHLYFSQSYGAFT

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						GESLAAEIEGTMRKKLSLDEESSLF KQKAQQKRVFDTVRIANDTRGRSIS FPALLPIPGSNRSSVIMTAKPFESGL QQTEDKSLLNQGSSSEEVAGSSQK MGQPGPSGDSDLATALHRLSLRRQ NYLSEKQFFAEEWQRKIQVLADQK EGVSGCVTPTESLASLCTTQSEITDL SSASCLRGFMPEKLQIVKPLEGSQT LYHWQQLAQPNLGTILDPRPGVITK GFTQLPGDAIYHISDLEEDEEEGITF\ QVQQPLEVEEKLSTSKPVTGIFLPPI TSAGGPVTVATANPGK\CLSCTNST F/TLFTTCR/IYLHPSDIT\QVTPSSGV PFHLSCG\SSGSSFHSNTAVNSPALS YRLSIGESITNRRDSNYNLSVGTME VGPKFLQER\GIS\AKVYHSPI\SENPL QPLPK\SL\AIPSTPPNSPSHSPCPSPL PFEPRVHLSENFLASRPAETFLQEM YGLRPSRNPPDVGQLKMNLVDRLK RLGIARVVKNPGAQENGRCQEAEIG PQKPDSAVYLNSGSSLLGGLRRNQS LPVIMGSFAAPVCTSSPKMGVLKED
4577	10074	A	4875	1	638	LAWGGKGKGASSDSGGLVDSISTL TPTPGDTNT/HSDLIVRGGAYGGQW AHGVLAQVQPSVGAEVT\P*PQMGE *TDVCGSQQSPHICSLTLRVGATML GKAR\WKPLG*TLPR\KIV\NSKATC SPGGTAKVSAAIRGLGRCRVVTPTA ASFHSS*\WLVWKTGGSRRKKDSES WVNLTRTPIATAVPDMTTDSLGQIQ SIPGHPVLQPIDPGESL
4578	10075	A	4876	31	448	PKSLLSLLVKINYGYVPK*QATKAK LDNWDYIKLQSFCITTKIMNRVRRQ PAE*ENIFANQTSDKGLISKIYKELK QLNSKKANNLIKNWSDDLNR/HFSN EDIQMASRYMKKI\STSQIIREMQIK TTMRYHFMPIRMTT
4579	10076	A	4877	3	286	KFTFKRHHHLQLLKRK*DS*V*T*Q MFMEQIKEDLSKQRDNSCS*IGKLSI AKNIYVSI\IPG*FDAIPIKIPARFFYA FGLYCRNSVSLSPRLN
4580	10077	A	4878	3	236	ATHSTLPSFQGPVSLASMTVVGIDG KASRPLQTPLVCQLDQHSFLHS/FLV IPTCPVPLLG*GILTKLSASLTIPRLQ P
4581	10078	C	4879	206	262	MVAIGTGYRRPGLRTFLN*
4582	10079	A	4880	2	756	LTSSRGARPAPLRAPAR/LDPAFRAN PLSRSYGSGLPTFPYLHCSNMPKAC SPWRPAADMGT\PGARFTPSPPDFQ GPARAPPDAAGTATLSKARAPLSGR NPFQGRPCPSQRKENSPRSSRRTSPG SRRVTDTGRLAGAPCSATPDSGI*T RLPFRIGRGAPEAIAPSLRNGARPSL RTD*PMFQLLGYNWNPSPVRPSKV LRLNICYYTP\SHAPAAAPPGPADFQ GPARAHRTPPEPRRFPRHGPLSRGE P
4583	10080	A	4881	3	322	MGSVTGPLYSGYKEEVVCCTLVEV

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						FPSLLQVSRNPRMPFDFLGILIFCLG GQGFPRATTVSGHWPE*LSQSSSSP KLRPPTL*SKPAHPGAAEALKAVPR TSAGAR
4584	10081	C	4882	240	500	MQNGLSGAYFPSVWAAKDSQERR RSPATGRNDSPRAPLPRSSARRPSK ANLHTLGQLKLSSRCRAPRLRRAA RTRSXSDQXWRRXTT*
4585	10082	A	4883	22	696	CTFGSFPFPGLSAWSFRASLPPAPAP GPNERFRSPGAGGFWGVDAAGQPA PAEVLGTALRASAAPGCAD*NPKKI KWHPG/SFCSPGEGMEILQQVCSKQ LPPCNLSKEDLLQNPYFSKLLLNLS QHVDESGLSLTLAKEQAQAWKEVR LHKTTWLRSEILHRVIQELLVDYYV KIQDTNVTSEDKKFHETLEQRLLVT ELMRLLSPSQEREIPPLLGLEKADLL E
4586	10083	A	4884	1	594	AVVHFRLLPLPGPFILCLSGPRFPQP AAPGPNERFRSPGAGGFWGVDAAG QPSPAEVLGTALRAPAAPG\LQVCF KGSAGGASGKRSSGRVIPA/MWPET VVALGNPWTVQTEGKVGAGEPVL HFDSSRAL*GSVSCENNL*NQFNRS SCSV*RQALRI*KTPESEHLKCLGPC SSVFNTSECRRVENRSLNCPFTPCNL
4587	10084	A	4885	2	326	VKTAEFVNKWQKNSTKLWNSQAQI DSSSLVNQINDLRQTEIWMGDRIMN LESRIQMQCDWNTSDFCVTPQ\YNE TEH*WKKVKRHLEGREENLTL*IVK LKEQDFEASQ
4588	10085	A	4886	2	373	VLLTPEERTVVIALWRKVNVYALC R*GAWA**L*AYPWTHR\FFESFGDI DSSDAVMGKPIVNAHGKNVLGAFS DGQSHLDNLLGTYSQLSELHCDKL HVDPENFKLLGNVLVCVLARNFGK EF
4589	10086	A	4887	3	332	HLSIINLNVNQLNSPLKAYTLPVWIP SS\RGPTICCLQEIHFASKNTYKLKV KELSSSFQANEKEKHADKTGFK\PK L*REKNGHYIMIKRSVQKENIYIYM FLIADPDIC
4590	10087	A	4889	1	304	HSCSSMRMPPLPTPPP/IVLCPPHPSP LIKALVSSKPP*VPSPAETWPVAAL GA*VPAVLGWPLHTENVLPVPPLPL EMPRIQWHFMLCSFPQRSPRADEST
4591	10088	A	4890	1	254	RPRRQFGIEGSFLNQIKNIYKKSTAN VILYVDRLNAFSLISGSSSSSSSSSSS SSSSS*LPVNIIRQ/EKVI*GMQIVKEE LNLSL
4592	10089	A	4891	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRSL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCLSLPSSWDYRRPP PRLANFFVFSVETGF\TVSARMVSIS *PRDPPASASQSAGDTGVSQAPV
4593	10090	A	4892	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS

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						GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFFCS/RD TVSLCYPGWSRVA*SRITATSA\PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCLSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFIYLFIYFHRDEGSLCCPGWS* TPELK
4594	10091	C	4893	40	180	MSFEAEIVLSPDRTTALHPGLQIETL SHIIIILILSTISFHQLLH*
4595	10092	C	4894	4827	5060	MWIYFWTLNSVPVIYMSTLMSIPHY FDYCCFIVSDIMLPEITFSTFILLLMV ALAIRGPLHFRRHFRINLSIATKNA*
4596	10093	A	4895	2	311	FILHVCDKLILFVSGDTFQTVSPRFL APRTFLAPLQNP*PLSPCAVHISFSRP LPARSPLPP/PRPPPPPTCSTAIPAPTH NPILTTHSTPPPTLPTINLTSSP
4597	10094	A	4896	2	374	DLTPKV*SRKGKIGKLDFIRTKTFW SAKDHVKRLKRQTTDWEKIFLNHIS NK/GLLSRIYK*LQTQY*KTPSNPI/K KTAKDVKEHFTEEDIQMACNPMKR CSTSLAVRELQIKTTVRYLKIEFNF
4598	10095	A	4897	1	684	
4599	10096	A	4898	1	1349	
4600	10097	A	4899	1	821	MLQTWSGYDNPRVTQKVPPFQLNC LPMTVVLLILYAEVATDWNRVGLT QGQLLHSLRLDPWSGLTQRTFPTGA MEISPDYLPPEFIVENTERIDEREKG REQPPKKTPENKAWPKMLKGKKA KGKKVAPAPAVVKKQEAKKVVNP LFEERPKNFGIGQDIQPKRDLTRFVK. WPRYIRLQQQRAILYKRLKVPPAIN QFTQALDRQTATQLLKLAHKYRPE T\SKRRRLLAQAEKKAAGKG/VRPT KR/PPVL*AGVNTVTTLVENKEAQL DLYCAI
4601	10098	A	4900	1	868	GTRPKMPKGKKAKGKKVAPAPAV VKKQEG\LAKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVK\WPRYIRLQR \QRAILYKRLKVPPAIN\QFTQALGP RKQATQLA*AWPTKYRPRDKAREG SRDLFGPGPRKKAAWPKGTFPTKRP PVPSKQ\G*TTVTTLGGGPRKASAG WWIAHDVDF\LELGLSFLA\ALCRK NGGSPY\CIIKGKGQDWGRL\VNKK TCTTGRLSHR*TSED/NKALLLKLVE AIRTNYNDRYDEIRRHWGGNVLGP KSVARIAKLEKAKAKELATKLG
4602	10099	A	4901	145	745	RRRGTQSCNLITIVNHISEITVIMFIE CSLCIKVIRLFHLILLLDFSSKPAPPPP

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						PCGAPGL*TATLLSRLRTARDLGTR L*ASPASPLCAVPSPAAAAFL/SLPLP LCPSSSSARELRSPTPGLSGQPAPAA SPGPG/PAG/PPPPPPLAVRPRFAPHL QLCPGPPFSRPSVLPASSRCQPGLSA PSLPSSPRPPPLRGLGRS
4603	10100	A	4902	94	432	TFLFFLIFSSEYWKFQKKQYSLEKSL FVAYNHKDG*THFLKGNNQFIFSIA/ LFTLGDIIYCKDIFGRLGLQP/TDISSS DSPFLSFSSSIYILTWGQARWLTPVI PAFWEAKAG
4604	10101	A	4903	109	422	FFEDGVLSRSVAQAGV\QWR\NLSS LQPLPPRFK*FSCFSL\RSRWDYRHA PPCPA\FFVFLVET\GVTILARMVLIS *PRDPPASASQSAGITGVSHCAPSRH SLS
4605	10102	A	4904	3	364	HEETAYDINILS**TQTFNMARLE*N CCNTIKSISEK/PTANSIR*AKKQEGF FQISGIRQGCLLSSFLFIILEVLARGN R*DKN/GIQIGKKKVELSLFSETMRF NIWKRLWKPHITTRANK
4606	10103	A	4905	50	394	LSYSWHSIHLLMKIISWHFDGQFSA LVIL*LSVAVDTADYSHFLETASLL DFEFTVLSWFSSYLT/DMFLFTLVFS L\PFSIQLLNIGISQGSVLSPLLYYAS ASGYMSLNIMYRH
4607	10104	A	4906	49	366	SGSSLAAVFWGPKGPAQAP\GPWAP WASPSGPDLPRPLHPADPQRQRLST VPLPLSRPPALSLIAPMALSHSCSNIP P*TPPPASLRPESLTPARS/PPTR*SHS PPP
4608	10105	A	4907	119	246	FCFHHLNLPSLFLIF/NVCLCV*QSHS VTQAGEQWRNLGSLQPPPPRFKPFS CLSLPSS*DYRHAPPQLADFCISSRD GVSPCWPGWSQTPDLR
4609	10106	A	4908	1	280	ESRSVAQAGVLWRDLCSLQPPPPVF K*FSCLSLPSSWNYRCAPPCPASFFV FLVE\QGFTMLARLVLNS*PQ/CDPP TSASQSAGITGMSHCTWP
4610	10107	A	4909	406	661	SQTPDLR*SAHLSLPKCWDYRR/AA TAPGQNISFKLPNPWEKAKHLMKS T*RLKHFTNFALFV*NCIDD/WMEF ALVAQAGMQWHDLGSLQPLPPQFK WFSC\PASPKCWDYRREPPCPANFF FFLYF**RLGFTMLARVVSNS*PQ/C DPPTSASQSAGITGMSHCAWPFFFF LFFSFFFETGSHCVAQAGLK/PLKLK RSSCLGLRKCWDYRREPLRLAPSW TFRM
4611	10108	A	4910	3	459	ELRDGEKVLDLCAAPGGKLIALLQC ACPGYLHCNEYDSLRLRWLRQTLE SFIPQPLINVIKVSELDGRKMGDAQP EMFDKVLV\DAPCSNDRSWLFSSDS QKAS/W*DKSKEEFAFFYRLGC*GL QLRPLRPGGILVYSTCTLSKAENPR CDQ
4612	10109	A	4911	1	95	TPKVHASWQK/MAD*SGQCPVLQIP

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						LSSLSMMQ
4613	10110	A	4912	253	1531	SWKLAEKVWEAQLPGFPSPPQCSV RCGRGQRSRQVRCVGNNGDEVSEQ ECASSPPQPPSREACDMGPCTTAWF HSDWSSKCSAECGTGIQRRSVVCLG SGAALGPGQGEAGAGTGQSCPTGS RPPDMRACSLGPCERTWRWYTGP WGECSSECCSGTQRRDIICVSKLGT EFNVTSPSNCSHLPRPPALQPCQGQ ACQDRWFSTPWSPCSRSCQGGTQT REVQ/CA*APTRPSAPDALLNCGPPG SAPVNSQPC/MPAP**SMARDSSSTF APWVGTGPGFCVLPLLTQPPVCRSL RTCPGSGLPRIPPERGPGHLHGFLCH HRSPIGLGPLWNPLGSSSLFPGLQQ GMSSR*TEGVGKVNGTQSDFSGTV GQAHVGGCDGVCCTYCLRCCFWG LHGICVWSNVYHFSKRRLHRTLEG TRPVFLEDFS
4614	10111	A	4913	131	355	STADTLP**TPKLSPQLMDTILPSQS VAMFHT*DHSAPTG/TGAPPHTTPS RPLNTRGPTEEFSPRPPPQHRPSSC
4615	10112	A	4914	3	420	QQPPTRLD*GPKQLMPHSPHNPHTI* NPAVLSLPPQTKLLGPPVVRGPLLIR *SPQLLPACLPL*RSTRPGTLKPKAT PA\PPPTTVHKPVASLRSHLRADGPG APPHTTPSRPLNTRGPTEEFSPRPPP QHRPSPPPTK
4616	10113	A	4915	11	375	
4617	10114	A	4916	3	260	
4618	10115	A	4917	3	208	
4619	10116	A	4918	1	422	
4620	10117	A	4919	127	4348	GASISDIQTETTEEDSVLLMHTLLAA TKDSLAMDPPVVNRPKKSKTKKAPI KTITKAAPAAPPVPAANEIATNKPKI TWQALNLPVITQISQALPTTEVTNT QASSVTAQPKKANKMKRVTAKAA QGSQSPTGHEGGTIQLKSPLQVLKL PVISQNIHAPIANESASSQALITSIKP KKASKAKKAANKAIASATEVSLAA TATHTATTQGQITNETASIHTTAASI RTKKASKARKTIAKVINTDTEHIEA LNVTDAATRQIEASVVAIRPKKSKG KKAASRGPNSVSEISEAPLATQIVTN QALAATLRVKRGSRARKAATKARA TESQTPNADQGAQAKIASAQTNVS ALETQVAAAVQALADDYLAQLSLE PTTRTRGKRNRKSKHLNGDERSGS NYRRIPWGRRPAPPRDVAILQERAN KLVKYLLVKDQTKIPIKRSDMLRDV IQEYDEYFPEIIERASYTLEKMFRVN LKEIDKQSSLE\ILISTQESSAGILGTT KDTPKLGLLMVILSVIFMNGNKASE AVIWEVLRKLGLRPGVRHSLFGEV RKLITDEFVKQKYLEYKRVPNSRPP EYEFFWGLRSYHETSKMKVLKFAC RVQKKDPKDWAVQYREAVEMEVQ AAAVAVAEAEARAEARAQMGIGEE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AVAGPWNWDDMDIDCLTREELGD DAQAWSRFSFEIEARAQENADAST NVNFSRGASTRAGFSDGASISFNGA PSSSGGFSGGPGITFGVAPSTSASFS NTASISFGGTLSTSSSFSSAASISFGC AHSTSTSFSSEASISFGGMPCTSASFS GGVSSSFSGPLSTSATFSGGASSGFG GTLSTTAGFSGVLSTSTSFGSAPTTS TVFSSALSTSTGFGGILSTSVCFGGS PSSSGSFGGTLSTSICFGGSPCTSTGF GGTLSTSVSFGGSSSTSANFGGTLST SICFDGSPSTGAGFGGALNTSASFGS VLNTSTGFGGAMSTSADFGGTLSTS VCFGGSPGTSVSFGSALNTNAGYG GAVSTNTDFGGTLSTSVCFGGSPST SAGFGGALNTNASFGCAVSTSASFS GAVSTSACFSGAPITNPGFGGAFSTS AGFGGALSTAADFGGTPSNSIGFGA APSTSVSFGGAHGTSLCFGGAPSTS LCFGSASNTNLCFGGPPSTSACFSG ATSPSFCDGPSTSTGFSFGNGLSTNA GFGGGLNTSAGFGGGLGTSAGFSG GLSTSSGFDGGLGTSAGFGGGPGTS TGFGGGLGTSAGFSGGLGTSAGFG GGLVTSDGFGGGLGTNASFGSTLGT SAGFSGGLSTSDGFGSRPNASFDRG LSTIIGFGSGSNTSTGFTGEPSTSTGF SSGPSSIVGFSGGPSTGVGFCSGPST SGFSGGPSTGAGFGGGPNTGAGFG GGPSTSAGFGSGAA\SLGACGFSYG
4621	10118	A	4920	3	1380	NMLGKYL*VKDQTKIPIKRSHMLR DVIQEYDEYFPKIIERASYTLEKKFR VNLKEIDKHSSSYILISTQESSAGILG TTKDTPKLGLLMVILSVIFMNGNKA SEAVIWEVLRKLGL/RPGV*LGSLSA CCPCCPLAREDGPRIASVWWSGGT GWGAGLGRGPRVLTCVDDGQMVL KLSAVSLLNVLCLF*A*MLDRPSRIP DKEGIWVLNCLLLVAMCSLLSSLH* DCPMC*ERSPSMLGKWPLALNLGQ FLICGSWGLIFPNCQG*GIHSFGGSE GKLIT\DEFVKQKYL\EYKRVPNSRP P\EY\EFFWGLALPTTETSKM\KVLK FACRVQKKDPKDWAVQYREAVEM EVQAAAVAVAEAEARAEWFQHQH WLYLANPAPSNGASSSGPKFYCWL PAVDPSTGVGFCSGPKHQVASSGGP STGAGFGGGP\NTGAGFGGGPEHQC WLWQVEPPVLVPVAFL
4622	10119	A	4921	1	412	TRMGLPDASRRRTCRMDPEGWQE AMSSA*GRITLQRLSTG\PEGQGGRE KVGPEGGSENPQQPKAAGVLSKHL PGAPAQPPQRPPSSPPPLAGPLTERV EKVCDFLDAAGDYLN/GTPG*PSPG ESPAAQDPPVPPWPP
4623	10120	A	4922	117	295	
4624	10121	A	4923	1	3564	
4625	10122	A	4924	1	355	LPGIEVLWQGPKVVSKEIPVESIEEV

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						CKSIKRAPVIWDTIHVN/DF*SALTP YQIVTTKFYFRIKKIVHWGPFPHSSQ KILSICEKYQWLSVPLTHNLTKFLSII VNYSRYHCIKPQLV
4626	10123	A	4925	3	3145	AAAEGELGAWRGNSGRPKIIGRAA EAENEDRTLGRLLPGNERSQPRSPL MLLAPQLKAEAAADKGLAPVPPPF SSGHSGPCEREGEGQRGRGRSRRG AHLELKPSPGLRAGAPTDRGRGGP AEVAAAGGRRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAPGE DNPAGAGGAAVAGAAGGARRFLC GVVEGFYGRPWVMEQRKELFRRLQ KWELNTYLYAPKDDYKHRMFWRE MYSVEEAEQLMTLISAAREYEIEFIY AISPGLDITFSNPKEVSTLKRKLDQV SQFGCRSFALLFDDIDHNMCAADK EVFSSFAHAQVSITNEIYQYLGEPET FLFCPTEYCGTFCYPNVSQSPYLRT VGEKLLPGIEVLWTGPKVVSKEIPV ESIEEVSKIIKRAPVIWDNIHANDYD QKRLFLGPYKGRSTELIPRLKGVLT NPNCEFEANYVAIHTLATWYKSNM NG\VRKDVVMTDSEDSTVSIQIKLE NEGSDEDIETDVLYSPQMALKLALT EWLQEFGVPHQYSSRQVAHSGAKA SVVDGTPLVAAPSLNATTVVTTVY QEPIMSQGAALSGEPTTLTKEEEKK QPDEEPMDMVVEKQEETDHKNDN QILSEIVEAKMAEELKPMDTDKESI AESKSPEMSMQEDCISDIAPMQTDE QTNKEQFVPGPNEKPLYTAEPVTLE DLQLLADLFYLPYEHGPKGAQMLR EFQWLRANSSVVSVNCKGKDSEKI EEWRSRAAKFEEMCGLVMGMFTR LSNCANRTILYDMYSYVWDIKSIMS MVKSFVQWLGCRSHSSAQFLIGDQ EPWAFRGGLAGEFQRLLPIDGANDL FFQPPPLTPTSKVYTIRPYFPKDEAS VYKICREMYDDGVGLPFQSQPDLIG DKLVGGLLSLSLDYCFVLEDEDGIC GYALGTVDVTPFIKKCKISWIPFMQ EKYTKPNGDKELSEAEKIMLSFHEE QEVLPETFLANFPSLIKMDIHKKVT DPSVAKSMMACLLSSLKANGSRGA FCEVRPDDKRILEFYSKLGCFEIAK MEGFPKDVVILGRSL
4627	10124	A	4926	3	251	HERHELQMLVDAPCSDLAQELRQS CATVQRLQHTLQQVLD/Q/REEVRQ SKQLLQLYLLALYNEVSLLS*QDIF NVALDVCMCRS
4628	10125	A	4927	1	408	GTSLNSLSKTKAKDLFIGDVIHNAG PHRDKKLKYYIPEVVYSGLYPPYAG GG\GFLYSGHLALRLNHIADSVQF*P R*DPYTVR*LLKPSSAGYDPTFVLLI GTDGIYTYTPSSCENGLGSCEEPHL MSFRSYFHG
4629	10126	A	4928	187	378	LCQKTMSLFTHSFCFSVGRNMEGV

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						LMDVDCESVYPIV*ASN*GLASAEV GGSFEPRSLRPAWAT
4630	10127	A	4929	26	121	PDRTMGG\REQRQSPGAQRTFFQLL LSFFVES
4631	10128	A	4930	3	867	
4632	10129	A	4931	1	558	EVRVKCVKALKG\LYGIP\DLTACL KLFTGRFKDWMVSMIMDREYSVA VEAV\RLLILILK\NMEGVLMDVDCE SVYPI\V*ASI*GLASAVGEFLYWKL FYPECEIRTMGGREQRQSPGAQRTF FQLLL\SFFVESKSHFVTQGGGSGQF SAHRNLCLPGSGNFHVSASRVAGIA GAPPHTWLIYVFFS
4633	10130	B	4932	1	1617	MKNGVQWAELAGHDYVLDLVSDL ELLRDFPRQKSYFIVGTEGPAASRG GPKVVFGNSWDSDEDMSTRPQPQE HMPKVLDSDGYSSHNQDGTNGETE AQRGTATHQGQPTMAAVSESDSLG EPAVPHKGLDCYLDSLFDPVLSYGD ADLEKPTAIAYRMKGGGQPGGGSS SGTEDTPRRPPEPKPIPGLDASTLAL QQAFIHKQAVLLAREMTLQATALQ QQPLSAALRSLPAEKPPAPEAQPTS VGTGPPAKPVLLRATPKPLRPAPLA KAPRIPIKPVAAPVLAQDQASPETSL HRDAATVTQMHFLTGQGRLLSLLD DSSLHLWEIVHHNGCAHLEEALSFQ LPSRPGFDGASAPLSLTRVTVVLLV AAGDIAALGTEGSSVFFLDVTTLTL LEGQTLAPGEVLRSVPDDYRCGKA LGPVESLQGHLRDPTKILIGYSRGLL VIWNQASQCVDHIFLGNQQLESLC WGRDSSTVVSSHSDGSYAVWSVDA GSFPTLQPTVATTPYGRACTPVAHD HIDELVRGAVFSEKHFCIEDL*
4634	10131	A	4933	1	811	HASAGAGCWHLPGIIEGAAQGKGR GRQVIAVARTADVIIMMLDATKGE VQRSLLEKELESVGIRLNKHKPNIYF KPKKGGGISFNSTVTLTQCSEKLVQ LILHEYKIFNAEVLFREDCSPDEFID VIVG\NRVYMPCLYVYNKIDQISM\E EVDRL\ARKPNSVGSSSCG\MKLNL\ DYLL\EMLW\EYL\ALT\CILHQGRR RDRRARFSQDAIILRKGASVEHVCH RIHR\SLASQFQVTPWVWGAPAPSY S\PQAGGALTH\TMEHEDVIQIVKK
4635	10132	A	4934	1	431	QRFPAAFPG\PGARRDAPPHSPPAEC RAHAATWRLKPRPHRPHSLTAPLP VHWAGTTEPLPSRPATGTESARRC ISGDTSQSFLRLARPCRQPGPS*DRC RPGVVSCLDREEKNAGHWLSMAFS LLWVLATQHCLHPEESLTM
4636	10133	A	4935	56	252	GAQERGCPREKHGNAELAEGLVLIL RGRGKPPSASLAGRE*I*SRGPEWK VTVNQTAKAKERTGP
4637	10134	A	4936	81	896	CGLVTPACLDPWVGIAPLPDTLIVL RGGGSALLPAPIPPVTLEEKQTLTRL LAARGATIQELNTIRKALSQLNGGG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LAQAAYPAQVVSLILSDVAGDPVE VIASGPTVASSHNVQDCLHILNRYG LRAALPRSVKTVLSRADSDPHGPHT CGHVLNVIIGSNVLALAEAPAAGRG TG\YQAVVLSAAMQGWGTPAAHR DDRYQCHGHPPLVPAASVMA*VTF WEFRGGLQGQGQMAEQARLADGG FPLPLRMRTSPSASSAFPCFSLGQPL S
4638	10135	A	4937	100	332	NKPQPQLLYRIKLTSTPFHPIQKVGL RQMIDLNIPPRIIKLLEENIK*YLSDL GV\TK*KLTKFNFLKIKHFCSPSSC
4639	10136	A	4938	692	900	NKLLWLGAVTPACNPSTLGG*GGQI MRSGVRDQPVQHGE\TWSLLKIQKL AGHGWPAPGSPSCLAGLRQE
4640	10137	A	4939	87	322	ARLVQNTGAQLKEVQYKLFFGFLF FE*/QSHSVAQAGYSAVIIAHCNLSL LGSSDPFFSAS*VAGTTGMCQHAW LIFDR
4641	10138	A	4940	91	356	GHAFLFGGYYSSSHWPSTYPPHAPV PPPPPS\PPYPSLPPFHSLPPIKPFPLPP /SPPSPPSPSL*SPPTPPPTLLIPSPSPPP ASPPLQ
4642	10139	A	4941	2	332	CGGPPGSPDTRGGSLIPQGV*AA\GP MEQVPLVAPSSAIPAVPGSLSGTPSH QPVLGTHTPSCPGLTYIPPPESSELP DCPAPGRQRPCPGQTPLPTPCPPSFI FSKQPRA
4643	10140	A	4942	637	1560	VWQLDKSMRAAQPWAPAGGAAGS EWAGLKR\RPLGWSSFSPAAAQSPL ELLGHPQPSPWPSEAPWKACQVSF QGT/RVAASYHNAQHGTERQHSSSC *GLGS*/CNSPTWARLSTHCPQ/HSR NTPRTQHCPHYPPRGLAKRWLCGE GPNPYSHPLREGPLRRRVGRGMGK EVHLFYRAWHSGIHFPS/TPSRTSHQ DSPHLEN*TSPLIDLTPTWAPPMCK RIL*KCTCNSLPQKPSMALQCI*NEI NKTSTTSPT\CLAPH*APATLACSPF LQPAELLPISGTLHVIFHPPRTLFPKS RTGSFLSSPQVSV
4644	10141	A	4943	2	335	ALHPTLTLDLYFTIYTKIHST*IVDL DVKPKTLKCLEESIR/VKLCDLRLSK ISWILKAQSIEEQTDTWDLKT*NNY SSNGTVKRIKRQVED\WHKVFARRI SDTGLVSRISC
4645	10142	A	4944	2	345	FFFFFFETESRSVAQAGVQWRDLSS LQAPPPG\SRHSLASAS*VAGTTGVC HHARLIF\VFLVETGFHHVSQDGLN LLTS*SAGLGLPKCWDSEKLFFFFG DKSFRFCCPGWSTMV
4646	10143	A	4945	178	388	RREPLHPANLLLFFFFFFEMESPSVA QAGVQWRDLSSLQAPPP\GSCHSPT SLS*VAGRLRNKNCLNPDAW
4647	10144	A	4946	546	850	FSVLFYFFESESCSVLQAGVQWRDL GSLQPPPP\GSSHSPTSAS*VAGTTGT CHHTQLIFIFLVETGFHHIGQASLKL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LTS*FAHLGLPKFWDYRCEPPHPA
4648	10145	A	4947	169	358	GNGFLFCTQVEVQGAFL*YLNLLAP GVK\LFSCLTLLKPWDSGTFPTFSFN FFIYLAEKGFNG
4649	10146	A	4948	1	145	ANSAAMPSLGCSASSGLVFWPQGL YLLGVVSVSPLPPTPTTVTFPEQI*LL SPQVSSSPVSEGSSQH\PA*SLRPFHV PRS/SPVSSLQPFAPAKSPGPSATCAF SAPSLSLLTLLASGDSSFWGPGPIQM SAGGSIVMCS*GLVFWPQGLYLLG VVSVSPLPPTPTTVTFPEQI
4650	10147	A	4949	1	295	GTSSRLRLHRTDELTAPSIYRSTKST LDGSLAANEREPFTLGKKPPFSDKP SIPAGRSLGEHLPKIQKPPLPPTTER HDWSRRLAGKKPPVPKHGWVP*/R EDDNE*DELTAPSIYRSTKSTLDGSL AANEREPFTLGKKPPFSDKPSIPAGR SLGEHLPKIQKPPLPPTTERHDWSR RLAGKKPPVPKHGWVP
4651	10148	A	4950	119	1036	HASCLKTQALQECSVGVGGGLPVS PAGPPRCFCPALPAAALALQGTFPA TGG*AWGLSSPDWTFSTKKLVMES ARSHGEGGAQGPATLTGPPGEGAL RASQ/PGTAGSELRHRARGPAQICST RTR\PAPWWT*SLPPPGHSRAVGFD RCGPASP\GVPVNAAVALPPSTCGE ESRLPQEEGGIHMA/PGTPLCSGDCI CCED*PQSRSGQFGADSL*RAKGGT LPSGPSARRRSPL*ASESASCCRRAS S\GPPAAQGERADSRALGTAPPGEG LALRPTPGGIGTPPAGGSEDISREVD PAKRHGLGA
4652	10149	A	4951	2	1262	GSAAGSTYEPSSMRLEALQVLTLLA RGYFSMTQAYLMELGEVICKCMGE ADPSIQLHGAKLLEELGTGLIQQYK PDSTAAPDQRAPVFLVVMFWTMM LNGPFSRFSA\DSEHPTLQASACDAL SSILPEAFSNLPNDRQMLCITVLLGL NDSKNRLVKAATSRALGVYVLFPC LRQDVIFVADAANAILMSLEDKSLN VRAKAAWSLGNLTDTLIVNMETPD PSFQEEFSGLLLLKMLRSAIEASKDK DKLSTISIYYFNGQENRKEKNWNER EYKLEIPYELCTEVDAINKWTAPWT SQAYNALTSVVTSCKNFKVRIRSAA ALSVPGKREQYGSVDQYARIWNAL VTA\LQKSEDTIDFLEF\NTVSSLRTQ ICQ\ALIHLLKLG/RSASDLPL\MKET LELSGNMVQSYILQSLKSRSIGR
4653	10150	A	4952	52	730	KSACDALSSILPEAFRNLPNDRQML CITVLLGLNDSKNRLVKAATSR\AL GVYVLFPCLRQDVIFVADAANAMV MSLEDKSLNVRAKAAWSLGNLTDT LIVNMETPDPSFQGRVLWSPALENG YDQALEASKDKDKVKRH\AV\RAL GNLLHFLQPSHI/GKTPHLQKFI*GSL SRALNFLLF*QKLAMKVRWNACYA MGNVFKNPALPLGTAPWTSQAYNA

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LTSVVTS
4654	10151	A	4953	3	363	HELEFEIKNTIPFILAP/N/NIKYLGIT/ LTKYVLYLN/DLYAENYKTLMK*IR DLNGDPLSCKVKNLIKINKYMK\EIL CSRIGKDSNIV*VSLLPQL\ACRLNAI PIKIPANHFVEVN*LILKFI
4655	10152	A	4954	179	438	ENIMSKTSTENCTKQCHFWHVNI*Y SIFFFFLRQSL/DSVTQAGVQWRHLG SLQAPPPGFTPFSRFSLPSSWDYRCP PTSLANFFCILVETGF\TVLARMVSIS *PRAPPASAS*SARCKLHLPGSHRSP ASASPVAGTTGARQQAWLIFFVF
4656	10153	A	4955	1	264	QFPKPSPRGP/TPTKSLFHILSPPNQ*I SPPP*QLPPSLYQIPPTIRLSPLPLAES PSPLSVGLGGPLGWVGQLLCLSFPG GPKHVEV
4657	10154	A	4956	3	369	HERHELVKEFNKVSGYKINAHKSV ALLYTN/DDQAENQIKSSTPFTIAAK SVK/YLGIYLTKEVKDLYKENYKTL LKEIVDNTNKRKHIP*P*MGRINIVK MTTLPKAIYKFNSMPIKISPSHFG
4658	10155	A	4957	2	338	GCWDN*ISTCKRMKLDCSLMLHMK INSM/WIKDVNIKSSSYEK\NIGVNLP DNVLGNGFINMMPKAQASKEKIIN WDSAKLK/IRK*RQLTEWEKLCANP IYSHLIPVLCYLYLV
4659	10156	A	4958	42	447	IELVTVLQFYRAFYLFERYAGFLFY YYFLFFVEIRFHYIFQAGLS/ELLGSS DPPTSGLPKCWDYRR\DHRTWPDM QDFLMFHIFPKLFSFPDMCFLASE*P SANTWLLLVVQSSFSLLSHTYHPPG KASTLWFSA
4660	10157	A	4959	377	1220	FRKVVPLAESHPAVPG\GKVRTSRS PKSPPRALPT*/PGLFNPGCQRETPSP LG/PPGQHP/VPGQLNSKRKQIPHNE LVEQTLRSGLTSAQPAHTGGYSCS KLRPGPLPNPNGLCRCSDGRIPGDR EPLALSRT*IHLRACTGPDAAAQVL PGLLPCPPHLPPHLSGMFDSWLAPP LPDPCQRPTPPQAPSSEANNQRSQA PGCGPHSLRDSELQGQCPGPAQAFC RGSGLFQLTQLTGPLHGTR*RLSPK NSQALKPHM*AVGRILHWPPAARP GNSGRYPDD
4661	10158	A	4960	3	353	HEVPAKGPRPHLTDCPTTQDFLPGF SPRPASGPPPPSLSLRLFQQPG*TVW SPGPPCPVVPDCTSASGQVPFLPPAF RFKNVF*PSRPSPGTRGGP/PP*VCTS R/PLP*TSEPQPQPG
4662	10159	A	4961	301	343	TRMAHFWS*STKPSPMGPIQWSHM PGAFSE\SSSCHSHSAFLPPYFSHGPS NRPPIRALCRNLPLPLPNKPRAPSAA DEDNSLNVEWYVPYITRPQA*AALI KINQDGTFLVRDSSKK
4663	10160	A	4962	2	319	ARGPGPSGKSGARSGLGNTPRRGG AGLGRVPWSLCY*EGVESGRPEGA GPGTSPGVGFIGAYHGRGVTKVGG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPG/GQACGVWSDPKSPGEPVEPIPG GSWPPQREP
4664	10161	C	4963	109	372	MQAWINIRKSVYVIHCVNKIKXXX XXXXXXXXXXXXXXXXXXXXXXXX XKLRRELPQPVKGHLQKPMADIPN GKKLKASTTKIMNKTSS*
4665	10162	A	4964	3	990	RTLRECYK/HI*ANELNNLDEMSKL KDA/TLLQLTQEEIETLKYNNEIE*I M/NKLPTKKSPGPHGFTG*FYQMFQ EEFTPILSRL**KIKEEGTVPNLLYEV /SIIMIPKPDKDITRPVSLMIIGAKIFK QNI*HTQVYAHIHRIV\YHDHNGFM QAWFNI*KSVYVIHCVNRIKDKNH MIVSIGA/EKAFDKIQHPFMVKTKT QERTF/FILLKGIY/NKPMADIPNGKK LKA\LPLRSGTRRVPDRFWKWQ/CP LPLLFSIVLEVLARAVRQEKEIKGM QIRKVVKLFTDGMILYVEKSKESTI KTSKLINRFNKGSEYKANIKK*VVF L*SSNQQTK
4666	10163	A	4965	3	314	HENDSNPETDNRQEGPSQENIGRVS D/MAFVPSAWTASGGVAWGNPGES GSRTGGVRAETLAPRLQV*PAHLIG HPRSNRGQGRPPWKAGKLGKCQEV LFRFAAF
4667	10164	A	4966	2	329	ARGEECRKAFRCIYDCVIHE/CEECR KAFRCIYDCVIHERIHNGEKLYEC*E CETSLSSNSVLIQHQRIHTAEKPYEC NECGKAFHRTSVFLQHQRFHTGEQ LYKCNECWKTFRCSSRFIVHQRIHN G*KPYECNECGKAFHRTSVFLQHQ RFHTGEQLYKCNECWKTFRCSSRFI VHQRIHNG
4668	10165	A	4967	61	533	WTEPVRHPDIHSQKREPSLMPPTVT GPGTTNMLFQPHRGPEKSRVPLHSS SSSSSSSSSSSSSSSSSSSPKTF/FGAPK/LP PSAPTSPDLAQAS*GLKSWKPWSGE RRFGCSKQRRALPTAS*FQGQSHAA PETPSYVGQDQSPSPGG*RPSTSPEG DSCFP
4669	10166	A	4968	22	482	GKGPGPPGGVCKSTLPPAKPWRGPP HLPLPLGL*EKALPRALGQWEGRES FWDQPGKLPLQN/PPRSLGVAMGT QAVEIPDGRLPDLSPTPAHSFSFLAL KPLLGEARVHFRASAWPLPTRAWT LDLPQLGWGFWDCMALALESRSSG ESPSLL
4670	10167	A	4969	146	1299	GAPGPWPTGTTWLPGAAGAVPDPG FLLPSSAALSRSTAS*FSQPPPVPPAL TVPWPRCGC*TSCPAVPQPSP/GLPR TLVPACRGLPLSSVPSSPASRPKLPL HSPSSWSIPPEGSWGPLPTTLPLPWG L/PRLQSREHKPALSAATWQGLVVD PSPHPLLAFPLLSSAQVHF*PGLRSW VGPFFGLRKQP*HTGLSSLTTGCCP AWLTSWPRISQSERKAHP*CLPL*Q ALSPPISYFNLTVDLRNRDYHSASSS SSSSSSSSSSSSSSSRRLSWSPKHHPL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPSFILSWPQGIPRGLKNPGKTRGGL GWWKKGFLANWLSKKPRRKKGPS FPPLVL*FQGPRALPVPRNPHPKLG ASSQSPSPWWGKRPKPKSPGNGTS WLPPK
4671	10168	A	4970	298	954	QVQGHEDFLGARNTTLCSSFSCPGP GILGAEILETVGWCEKVCMLRAEK GSPHCFVIPGPEPCSPRNPNLAGAGP ESKPWWVEAKQKP*SGLLLPLVVFS VPRS*NCEPGVGERSGRG\HLGFLQP GYP*PHQGFWEILQGQLSRLFPNSSL PPH/MPLKPQQKSHSSHKQKGRGKN EEKTLCQVICRQRMGLVP*QHPTPC GAPPSPHHPQTPPKQVPYL
4672	10169	A	4971	4	410	PIERPHELKHRLPHVQKLVEDVGDG VIPAALEEGQAGWSHGFLVFLVEIK SAEGP/PGPADSRVRGVRPQRSQSA GPA*RAGRQDGVCRSLGQGRGGGR ATSLVLHPPGYPGCWFSVGVPSLPQ YTGIRSSSPRTRG
4673	10170	A	4972	148	268	LQPR*PLTCAPPPCPVQTQTHPISVS QTLLGLEFCCSLSL
4674	10171	A	4973	397	1449	RSHPSGTGRRTSRLESWFLGVSCKK SKVREGPLGPA**AG*RGVRPQRSQ SAGPA*RAGKRQDGG/SPEPRAGVG GEVGTQSP/GPSGASGYPGMLVSKP VGGTSASWLPAGCPIPS*LS*QRSQG SPSSCLIGHLLALWAAFGLGVTSLP QYTGIRSSSPTA*ATVQGDSGHKGG TGGTGLGRGRNTQPDAACGRGHRS SPTR/RPHGNPNGNTGCAEGGQARS LLPKLAPKLPGWPVSVPVAVG\PGD FGWRQAQYQSSLWDLSSPRNTLGR SATSAGPAPPALLGAGSGRSSGTSP AAPGCSSRCHCWASAPAGVSGGPG\ GRGAEAPPSPTLAQRGSPPG\AAIFP PACGIPP
4675	10172	A	4974	2	637	ARAKEV*DLYTERTK/PLLKEIKEDR NKWKHTSCLWIARLNIVKMSILCKL VHRLSAITIKI/PCWLCLAEIDKLILK/ FIWKFK/RSRVAKTVLKKKRKVRRL TLSNFKTYYFRVTVIKIEWLWQKD KYIDQWNRIKSLEINSYICGLLIFYK SAKTIS*ENSVSWYLDNWIPTCERM KLAPYIIYKKIK\WIKDLNIRAITVKL IKENIGPGARL
4676	10173	A	4975	254	590	KARYILPDLMIGLDFFFFFLGETKFP FAPQPGGHQGDLG*LKLTPPRDFP/C LTPPRSGNYRLGPPPPLNFFVF*KKR GGPHVGQTGFELLT*KDPPPLASQR AEITGGTHHA
4677	10174	A	4976	103	378	CFLYSICRGADTQRRFKLSDLSINST ECLHVHCRGLEISLADCAYT*ILTK GNHNPLS*YTFMRN\AKQPVN*YHR CTETFSLTRMELLVSV
4678	10175	A	4977	2	327	RQCLALWPRLECSGVIIAHHSLHLL GSSDPPTSAS*VAGTTGMHHHAQLI/ LFWVLIDTG*CYVAQTGLEPLNSGH

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PPTSASQSAGIIGLRHRAQPCVFQSS QKRGPELF
4679	10176	A	4978	19	1009	KTTQQQQNLFFSSAHET\FTNTDHIL GHETSFDMF*HIQVI*STFLYHNVIK LEVNSRKISGKCPNMWKLNNTVLS NTKIINFLDNKQNETIKI/RAETNELE NR/RTEKIN*TKM*FFEMINTIDKSL AR*SRGKRHKLLISGMTNVVSHCVS LPTLFLFQSCFDYILTTLHFLINF/QN RFNNLYKMIRGY*QLYKN*FDKLH EMKNFL*/RY*LPILTQEEI/S/HLNSPI YILKIEIVVLNLPTNKTYW*TLKF/EE MIPIVHRLFQKQETLPNPFYEVSITPI PKI/QD/D*TKENFRPISL\VDAKIPSK NLSNYICSRLNNASHPQRSTDPNLQ NF
4680	10177	A	4979	3	358	STSNAYHSNSLHQQIKEKKNHTILSI DAEKAFYKIQEPLLAITL*NRNSGN/ FLNMLMTTY**PKVNVILIGNTIPY* YFAFLLP*KLRTRQSRLSSLFNIVLK NPANVTVISINIKRK
4681	10178	A	4980	3	341	FFETESNSVAQAGVQWHDLGSLQP PSPG\SSNSPASASRVAGITGACPNV QLISVGFLFFVFWFFFETESLSVAQA TGVQWVRSWAYCNLRLPGSGRFLC LCLPSSWGLQGVR
4682	10179	A	4981	658	1001	LILSARPPKGEKGSFLLAEFSSYFHS GLFSSARSFFFFFFFFFETESHCVAQA GVQWLDLGSLQPPPPG\SSNSPASAS QVAGTTGVCHHAQLIFVLLVETGF HHVGQAGLELLTS
4683	10180	A	4982	53	394	PQQSGFWFIYFSKQGCPFFVNILNIC SFVLFFFFETESCSVAQAGVQWHDL GSLQPPPPG\SSDSPASASRVAGITG ACHQTWLIFVFLVDMGFRHVGQAS LKLLTSGFKKWVT
4684	10181	A	4983	66	516	HFYQFFPHFSGRMDLWSSLLCHFF MTSQFVTFVFLLYFIFVVYILSV*LD F*MRKQT*LISG*ASI*YRYV*LQNL YVLKLYITPLSL*AHVLIYL/CYLKS ESHSVTQAGVQSHNLSSLPPRFK*FP CLSLPNG*DYRNVPPHPANFCIS
4685	10182	A	4984	3	324	HENRMKYEISINMWKLNNIFLNKL WVKEITSRLQKYFECSENKTTTYQK L*DAK\KMNQCQGYLWVFMALSA* ISKRKRLLINYLSFYLSKLEK*EPTK PKASSRKVV
4686	10183	A	4985	108	277	ARVIRRANFCIFGKDRVSPCCPG/W/ SPELPGLKRSPSLSLPKCWDYP*AT APGQHPYS
4687	10184	A	4986	29	454	
4688	10185	A	4987	116	424	
4689	10186	A	4988	1	1217	PPTTCTPACQGLSGAAMKSLVLLLC LAQLWGWHSAPHGPGLIYRQPNCD DPETEEAALVAIDYINQNLPWGYK HTLNQIDEVKVWPQQPSGELFEIED TLETTCHVLDPTPVARCSVRQLKEH

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AVEGDCDFQLLKLDGKFSVVYAKC D\SSQDSAEDVRKVCQDCPLLAPLN\ DTRVAHAEKAALAAFNAQNNGS\N FQLEEISR\AQLVPL\PPS\TYV\EFTV SG\TDCVAK\EATEAAKCN\LLAEKA IMAFVKATLK*ESLGGGRRLQLTCT VF\QTQPCDLHSPNPEGANEAVPTP VV\DP\DAPPSPPLG\APG\LPP\AGSP PELPCFYWAAPPG\HQ\LHR\AHY\D LR\HTFHGVWVFIGGHPSGRKCSHP PGKHGTVGSSLVFWCCCCLGPVVP SIVPG\RIRHFKVLG
4690	10187	A	4989	1	443	KKFVIPDFEEFTGHVGRIFEDVKELT GGKVAAYIPQLAKSNPDLWGVSLC TVDGQRHSVGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIVVS SLIKMDCNKAEKFDFVLQHLNKK
4691	10188	A	4990	3	217	ATKRKKKMKDKDKA\KLLEAMGTS KTNEEDKRRGLDKRTPDQAAFEKM QEKRDFSRHLDTLTEHYDIPKVHH
4692	10189	A	4991	3	475	AASTESGMVAYYQVQKGPLKLKG VAKLGVTK/RVRPEGPRDSVFIPLKP FLGTPGPDPPTRRLLMFFSRKKKKK DKDKAK\LLEAMGT\SKKN\EEEKR RGL\DKRTPAQAAFEKMQEKRHME RILMKA\SKTHKQRVEDFNRHLGTL \TEHY\DIPKV\TWTK
4693	10190	A	4992	783	5158	PDKSGRRRDVEGGVCCFLSLLRNSR YLLSTHILERGKKASLCHPGWNAL VPSPLTAASASWVQVILLPLSLPSG WDYSLLHLEELTGESPTSERAFNYH PTTCLRRKILQDSEHTASTRGPMTL DRPGEGATMLKTFTVLLFCIRMSLG MTSIVMDPQPELWIESNYPQAPWE NITLWCRSPSRISSKFLLLKDKTQMT WIRPSHKTFQVSFLIGALTESNAGL YRCCYWKETGWSKPSKVLELEAPG QLPKPIFWIQAETPALPGCNVNILCH GWLQDLVFMLFKEGYAEPVDYQV PTGTMAIFSIDNLTPEDEGVYICRTH I\QILP\TLWSEPSNPLKLVVAGLYPK PTLTAHPGPIMAPGESLNLRCQGPIY GMTFALMRVEDLEKSFYHKKTIKN EANFFFQSLKIQDTGHYLCFYYDAS YRGSLLSDVLKIWVTDTFPKTWLL ARPSAVVQMGQNVSLRCRGPVDG VGLALYKKGEDKPLQFLDATSIDD NTSFFLNNVTYSDTGIYSCHYLLTW KTSIRMPSHNTVELMVVDKPPKPSL SAWPSTVFKLGKAITLQCRVSHPVL EFSLEWEERETFQRFSVNGDFIISNV DGKGTGTYSCSYRVETHPNMWSHR SEPLKLMGPAGYLTWNYVLNEAIR LSLIMQLVALLLVVLWIRWKCRRL RIREAWLLGTAGGVTMLFIVTALLC CGLCNGVLIEETEIVMPTPKPELWA ETNFPLAPWKNLTLWCRSPSGSTKE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FVLLKDGTGWIATRPASEQVRAAFP LGALTQSHTGSYHCHSWEEMAVSE PSEALELVGTDILPKPVISASPTIRGQ ELQLRCKGWLAGMGFALYKEGEQ EPVQQLGAVGREAFFTIQRMEDKD EGNYSCRTHTEKLPFKWSEPSEPLE LVIKEMYPKPFFKTWASPVVTPGAR VTFNCSTPHQHMSFILYKDGSEIASS DRSWASPGASAAHFLIISVGIGDGG NYSCRYYDFSIWSEPSDPVELVVTE FYPKPTLLAQPGPVVFPGKSVILRC QGTFQGMRFALLQEGAHVPLQFRS VSGNSADFLLHTVGAEDSGNYSCIY YETTMSNRGSYLSMPLMIWVTDTF PKPWLFAEPSSVVPMGQNVTLWCR GPVHGVGYILHKEGEATSMQLWGS TSNDGAFPITNISGTSMGRYSCCYH PDWTSSIKIQPSNTLELLVTGLLPKP SLLAQPGPMVAPGENMTLQCQGEL PDSTFVLLKEGAQEPLEQQRPSGYR ADFWMPAVRGEDSGIYSCVYYLDS TPFAASNHSDSLEIWVTDKPPKPSLS AWPSTMFKLGKDITLQCRGPLPGVE FVLEHDGEEAPQQFSEDGDFVINNV EGKGIGNYSCSYRLQAYPDIWSEPS DPLELVGAAGPVAQECTVGNIVRSS LIVVVVVALGVVLAIEWKKWPRLR TRGSETDGRDQTIALEECNQEGEPG TPANSPSSTSQRISVELPVPI
4694	10191	A	4993	1	369	GTFQLPKPIFWIEAETPALPGCNVNI LC\HGWLQDLVFMLFKEGYAKPVD YQVPTG\TMAIFSIDNLTPE\DEGVYI CRTHIQMLPTLW\SEPSNPL\KLVVA GGCGLWLLASGNCCPRYHGWLS
4695	10192	A	4994	183	429	ISIKSMKLISDYKYCIYIYRYHRDVI RLGIIDIYSVLHPTSAQYTFFSSLHGT LTTRDNILGHKT\LNKFKRIEIRQYL FSDQ
4696	10193	A	4995	2	270	TSGCLQGSCC\TGPPGAVGRASRSR PSTRPPSRARPLGSPGCSARAQDAA DLPLPPPPPCCSPSSAGCRCSLGCF RRCPLRSSRRSRF
4697	10194	A	4996	1	428	NPCLSERQGCCEKLPLERSSTPQDS AGHPVT/HAHCSLPSPVDLCPLLLAT HRISCWHCQDEVQGGTD\SADTGD LEALSLLAGHGDTDGHIILDVPDGA PYPQRTKAGIDHLHQKILKIIEQITIE HEARDDNAPDYPKLANN
4698	10195	A	4997	131	412	RKWLKLLPCSFFSSKNIYAETFSPCV CIRVCIHVCVYTCVYTCVCIHVCSC PC/VGQASALKSVSLCQLHCILVLTP MLTLRFDKKFFTQDSHFI
4699	10196	A	4998	2	175	KFTWKHKGPRIARN\ILKRKIKVEGF TLPNFKTYYKAAVTETVWYWHKD SGLDHFVLL
4700	10197	A	4999	2	175	KFTWNHKGPRIARNNLEKEN\KVEG FTLPNFKSYYKAAVTETVWYWHK DSGLDHFVLL

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4701	10198	A	5000	1	909	MVLEVSVSDRDAVWRLWRAPIGES QQRSLGFWSKVLPYSADNYFPFER QLLACYWALLETDRLTVGHQVTLQ PELPIMNWVLSDPSSHKVGHVHQH SIIKWKWYIRDQTRAGPEGTTTPVIT Q/WDAHEQSGLSGRDG\KGQRFVLT GVDTYSGYWFAYPAHNASAKTSIY GFTECLIHCHGIPHSIASDQGTLFTA KEVWQWAHAHGIHWSYHIPHHPIA AGLIEWWNGLLKSQLQCQLGDNTL QGWGKDLQKAMYSLNQRLIYSTVS PISRIHGSRNQRVEVEVAPLTITLSD PLAKFFFLLP
4702	10199	A	5001	1	1014	
4703	10200	A	5002	349	718	AGPEGTTTAECP/I/CQQQRPILSLRY GTISWG/DQSATWWQVDYIRTLLS WKWQSASAKTTIHGLTKCLIHHDIP HSIASD*GTCFMAKEVWQWYCFSH SQDSRVQESRGGIGSCTTHHHPCSF PN
4704	10201	A	5003	1	558	
4705	10202	A	5004	1	2205	MGAVFEALWQYSPELPKASVMVQ EASKAIGQCQSSAAKLRRSGKESVT EPWARVLGALEMAARLYKVTSGH CHGIHTPSWRCLCFSTGGKERHAH DLPHVTAQSQGHQGGQGKISRTALK EPTVHKVTASLSPVVATSPPQPMLP SDFPPLSEEINPMLPEATVIASPKEIA RQDNVDSPQEPPPTPQFSSRPITRLK SQWAPRGPECVIGIDILSSWQNPHIG SLTGRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVEISATIKDLK DTEAVTPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAVPD V/VSLLEQINTSPGTWFEWSPK\KAL QQVQAAVQAALPFGPYDPADPMVL EVSVADRDAIWSLWNAAIGESQRR PLGFWSKALLSSADNYSPFERQLLA SYWALVETERLTVGHQVTLRPELPI MNWVLSDPSSHKVSGAQQRSIIKLK WYIHDWVRAGPEGTTTSVITQWAH EQSGHGGRDGGHAWAQQHGLPLT KADLATATARIHRSRNQGVKVEVA PLTITPSDPLAKFLLLISATSTSLEVT VPEGEMLPPRDTTKIATFGTQTGFL ALQLADGLLWDLVIIPGKGKPSRDL VESPSPYSTYEGIDGWPDEPAPTAT KPPVMPAPALPPDTRSGSKAPTVPT PYPQMEHHQVQLASNNSNTEALGH LSPQSSWVQTPGQNSGPAIPNHLGK DMISPPQMAPAGVKWESQKY
4706	10203	A	5005	155	531	GNLWSVDLRPGTPLRQNFRGTIRQQ HSRFTKNHCSQTPLLIPRQTGSGVD LSKLQQTCS*GSCLVCTIDLANAFFS IPVHKA/HQKQFAFSWQ\YTFTVLPR LTWLQPC*VPNLPAAETNTEPSNGT
4707	10204	A	5006	1	518	MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP

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						VHKAQQKQFAFSWQGQQYTFTVLP QWYINSPALCHNLIRRDLDCFSLPL DITLVHYIDDIMLIGSTIKWVVHSS/ DSIIKWKWYVHDWARAGPEGTTN GLAG*SGTCKKHEWKTGDKGIRGR G
4708	10205	A	5007	1	2592	MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCWRMTVDYC KLTQVMTPIAAVVPDVVSLLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQHLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEKALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDPSR HKVGHAQQHSIIKLKWYICDQARA VPEGTC*LNKEVAQMP/MGTTRKW TAAALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGTWKK HDWKTGDNEIWGRGIWMDCSEWS KTVKIFVSHAHEPSGHGGRDGGYA WAQEHELSFTKADLATGIVECPICQ QQRPTLSPRYGTIPQGQTFILTGINT YSIYGFAYPAHNASAKITIRGLTECL IHHHGIPHS/IVSD*GTHFTAKDV\ET RIHRPRNQGVEVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLLEGGT LPPGDPTTIPLNWKLRLPRGHFGLPL PLSQQAKKGVSVLAGVTDLDYQDE FSLLLHNRVTAAFPSLLHSSFAYLD NMIEKANKCHVEGVDHVSDPAQRR ECDRHTGSSCHLLRGPPQLQSQLVS GPRSPKSDSGESCLAWDPTFKAEVS PLAQGSPRNSVQEPSPRTGSPKSLLG ALIALWPSWYLSSDPDPQGSNSRNL EISACQKYLSPAFGNSDYSTAEDFN SDYTLKSPENSIGYARLEKHRRLYG GDGGDGGGDDVRGGKRGDDSASR KGVTERV
4709	10206	A	5008	1	942	MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSWRMTVDYCK LNQVVTPIAAAVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDYF\LLLQDITLVHYI DDIMLIGSNDHKVGGAQQHSIIKWK LYIHDQAQTGPEGTTTSVIAQWAHE QSGPGSRDGGYAWAQQHGLPLTK ADLATTTAECPVCQQQRPTLSPRYG TIPSLPLTKALTLQLKKCSSGPMLM EFTGLAMFPIILKQLD
4710	10207	A	5009	1	1795	MRKCGKPQFKLGQTNKANSRIQEE LIHSKSLIEQEGEKPVQFSAFHRMW QPADSQCDIIDSADIWADPLVRHREI

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						ITGSGGINRRRTRGGRGRGGEAAGG AENCGSREERERAGVGTAVTQLQN LNTIGIIGSRGGRGQVAAINHQRQG GHSYCKGQQKQNSNQNSVTHVEL WHWLINHSVPRSEIDRKPTTFLLNL YKQKTSRDLWPFTRVTLHRGKRND QTFQGLLDTGSELMLIPEDTKHHCG PPVKVEAYGGQVINGVLAQIQLTV GPVGSGTHPVVIYPVPECIIGIGILSS WQNPHIGSLTSRKTDGSWRMTVHY HKLNQMVTPIAAAIPDVVSLLEQVN TSPGSWYAAIDLANAFFFIPVHKAH QKQFAFSWQGQQYTFTVLPQGETL VNFSLPQDITLFHYIDDIMQIGSSDQ EVANTLDLLPRKSTTPSG/LYGFWR QHIS/HLGLLLTPIY*VTQKAA/SFEW GLEQEKALQQVQATVQASLPLGVY DPADPMVIEM/SLSDPSSHKVGCAQ QHSIIKWKRYVCDQA*ASPEGTS*L YCTSFIMEKEEVC/LSLEQTLTLDMG LPILHAMLLWIHLWIHGLPYPSSWY STQQCL
4711	10208	A	5010	3	169	DFQPFTRVTVHWGKGNDQTFRGLL DTGSELTLIPGDPKHHYGPPVKVG\ AYGAQLL
4712	10209	A	5011	1	562	
4713	10210	A	5012	3	591	DPADPMVLEVSEADRDA\VPISESQ QRPLGFWSKALPSSANNYSFFKRQL LACYWVLVEIEHLTMGHQVTMRPE LPIINCVLSDPCSHKVGHAQQHSIIK WRWYIHDWAEGTSKLHEEVAQIPM VSTPSLPQPAPMASWEVPYDQLTEE EKTRAWFTDGSARHAGATQKWTA VALQPLSGTSLQDSSEEKSSQWTEI
4714	10211	A	5013	2	586	
4715	10212	A	5014	3	514	
4716	10213	A	5015	1	994	MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCWRMTVDYC KLTQVMTPIAAVVPDVVSLLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQHLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEKALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDPSR HKVGHAQQHSIIKLKWYICDQARA VPEGTC*LNKEVAQMPM
4717	10214	A	5016	1	643	MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSWRMTVDYCK LNQVVTPIAAAVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDYF\LLLQDITLVHYI DDIMLIGSNDHKVGGAQQHSIIKWK

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						LYIHDQAQTGPEGT
4718	10215	A	5017	3	1074	VTASLSPVVATSPPQPMLPSDFPPLS EEINPMLPEATVIASPKEIARQDNVD SPQEPPPTPQFSSRPITRLKSQWAPR GPECVIGIDILSSWQNPHIGSLTGRV RAIMVGKAKWKPLELPLPRKIVNQ KQYHILGGTVEISATIKDLKDTEAV TPTTSPFNSPIWPVQKTDGSWRMTV DYCKLNQVVTPIAAAVPDV/VSLLE QINTSPGTWFEWSPK\KALQQVQAA VQAALPFGPYDPADPMVLEVSVAD RDAIWSLWNAAIGESQRRPLGFWS KALLSSADNYSPFERQLLASYWAL VETERLTVGHQVTLRPELPIMNWV LSDPSSHKVSGAQQRSIIKLKWYIH DWVRAGPEGT
4719	10216	A	5018	1	1482	MAPNSRVQELVLGQVAVICQGLLS LQPRTEGYTVGFLTFEVLDLTGSSA CRWPIVGLHSVIILLDKVTKEKDEL RDSNSWLQKQILSLKFSKTALSESLI SCRQRAEIVENQTQGLIMRPLAFHR GNCIGERGMTILFRGYWTEPTLIPED PKHHCSPPVKVRAYEDGSWKMTV DYHKLNQVMIPVTAAVPDVVSLLE KINTSPALFHNLVQRNLDCFSLPQDI TLVHYVDDIMLIGSSEQEVANTLDL LVRRLCAKGWEINLTKIQGPSSLVK FLGVQWCGASQDIPSKVKNKLLHL ALPTTKKEAQCLVGLFGFWKQLIPH LATPIIPQRAHEQSGHGGRNGGYTW AQQHGLPLTKADLATATAECPICQQ QRENGA/PRYGTIP\RGDQPATWWQ VDYVGPLPSWKGQQFVLTRIDTYS AYGFAYPTCNASAKTTIHSLTACLI HRHGIPHSIASDQGSHFTAKEVQQW AHAHGIHWSYHVPYYPEATGLIEW
4720	10217	A	5019	1	1494	
4721	10218	A	5020	101	304	
4722	10219	A	5021	1	1912	MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP VHKAQQKQFAFSWQGQQYTFTVLP QWYINSPALCHNLIRRDLDCFSLPL DITLVHYIDDIMLIG\PRQLLACY/W ALVETEHLTISHQVTMRPELPIMNW VLFDPSSHKVGCAQQHSIIKWKWY VHDWARAGPEGTTTPVISQWPHEQ CGHGGRDGGYAWAQQCRLPLTKA DLNTATAKRPICQQQRPTLSPQYGT IPQGDQPATWWWVDYMGSLPSWK GQRFVLTGIDTYSGYGFAYPACNAS AKTAICGLTECLIHHHDIPHSIASDQ GTHFMAKEVRQWAHDHGIHWSYH VSHHPEAAGLIEWWNGLLKSQLQC QLGDNTWQGWGKVLQKVVYALN QHPIYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLLPFPATLQSAGLE VLVPEEGTLPPGDTMIPLNWKLRLP PRHFGLLLPLNQQAKKGVTVLAGV

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						TDLDYKDEITLLLHNGGKEEYAWN TGDPLGLLLILPCPMIKVNGKLQQL KPEALVPKGVVFPPGDTTMLSLSW KLRLPSGHVGLLMPLSQQVQKGVT VLAGVIDPGHTSAASLVLRSCVWS GSDTIVSPGSQDFRLGINDTTGFPVF PD
4723	10220	A	5022	3	835	DLWPFTRVTVH/WGKANDQTFQGL LDTGSELTLIPGYPKRHCCPPVKVR VYGGQTDGSWRMTVGYHKLNQVV TPIAAAVPDVVSLLEQINTPPSTW\Y GQVAAFAPPTTKKEAQRLVGLFDF GGNTLLIWVYYSGPLSSDLKGCQFE WDPEQERLCKAFSAHSQWFGCQGL GRSVDWKIDDKKLGKRMRMDLSE LGKNREEYWYPVQQAKKGVKVLA VVIDQTIKMKSVYYFTMEKTCQRQ ATTAELEPEKNVIGVDETVEGQSYH SSKQKDIPFQGEK
4724	10221	A	5023	2	1300	DLWPFTRVTLHRGKRNDQTFQGLL DTGSELMLIPEDTKHHCGPPVKVEA YGGQVINGVLAQIQLTVGPVGSGT HPVVIYPVPECIIGIGILSSWQNPHIG SLTSRKTDGSWRMTVHYHKLNQM VTPIAAAIPDVVSLLEQVNTSPGSW YAAIDLANAFFFIPVHKAHQKQFAF SWQGQQYTFTVLHQGYINSPALYH NLIWRDLDRFSLPQDITLIHYIDDMT LIGSSEQDVANTLDLL/SDLSRGGF* *SSG*DDPFCGHHSASFPSHPCNRP MGP*TK*PWGQGWRLRMGSATCTP THQG*PGYGHC*VPNLPAAETNTKP SIWHHSSG*SASYQAAG*LYWTSFI MERAEVRP/TWSTCLLWIWVCLSCT QCFCQDYHLWTHGMPYPLSRYSAQ HCL*PRHSLYS*RSVAVGSCSWNSL VLPCSPSS*SSWI
4725	10222	A	5024	2	790	PRGRNRRRKTFQERRMTLNESPEKI GKWIECYGHPPASKLVEIYIHTVFV EDKLSICIRSFNKKADGSWRMTVD YCKLNQVVTAIAAAIPDVVSLLEQI NTSPDTWYAAIDLANALFSIPVHKG YINSLALCHNVIWRELDCFSLPRDT TLVHYIDDIMLIGSSVQEVENKLDL LVKDKLLHLAPPTTKEEVQHMVGL FGFWRQHIPHLGVLHQPIYRVIRKA A/SFEWGPEQEKALQQVQAAVGGK QSENNLGHQRSPGLWFS
4726	10223	A	5025	281	1461	VRVLSPVEKELKLWKNTHKLLSYP TVGAAVTQLQNLTAMGVIGSHGAR GQVVALNRQRQGDLQPFTRVTVH WGKG/NMQIFGGLLDTGSELTLIPG DPKHHCGPPVKVGAYGGQVINGVL AQVQITVGPQTHPVVISPVPECIIGID ILSSWQNPHIGSLTGIMVGKAKWK QLELPLPRKIVNQKPYCIPGGTVEIS ATIKDLKDAGVVIFTTSLFNSPIWPV QKTDGSWRMTVGYRRLNQVVTPIA

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						AAVPDVVSLLEQINTSPGTWYAAID MANAFFSIPVHKAHQKQFAFTWQG QQYAFTVLPQGYINSPALCHNLIWR DPDCFLLLQNITLLVHYVDDIMLIGS SEQEVANALDLLVFSDHLAIKWVM HSSIASSSGSGICVIRLKKVLKAQ
4727	10224	A	5026	1	3179	MAEDKEEQVPSYTDGSRQRENEED TRVKTPDKTIRSHETYSLPREQYGG NYAHDSIISHQVPPTTCGNYGSTIQD EIWVGDHSGYVRPVPVPRSLNSDIS YFGVGGKQAVFFVGQSARMISKPA DSQDVHELVLSKEDFEKKEKNKEAI YSGYIRNRKDDYDNHTGIDLVGTII ATIKGSNEEDTDTPLFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTDEKGR ANLGVFSVFAPRGEHTLQVKAIYN KSIIEGPIIKLMILPDPEKPVRLNVKY DKDASFLAGGLFTAPPLPAQLMSSL SCAWIIESVLNSWRKGCNKLRNQR ALHKKQDRGKLPEDRELQHTKKQT NWAGLLIPAMNNNVDMTARKLQR DLQPFTSVTVHCRKGNDQTFGGPL DAGSELTLIPGDPKHHCGPPVKVGA YGGQVINGVLA\HPLIWLVQKTDGS /WRMTVDYCKLNQVVIPIAAAVSD VVSLLEQINTSPGTWYAAIDLANAF FSIPVHKAQQKQFAFSWQGQQYTF TVLPQWYINSPALCHNLIRRDLDCF SLPLDITLVHYIDDIMLIGSSEQEVA NTLDLFVRHLRARGWEINPTKIQGP STSVKFLGFQWCGACQAIPSKMRD KLLHLVPPTTKKEAQCL\QLLACY/ WALVETEHLTISHQVTMRPELPIMN WVLFDPSSHKVGCAQQHSIIKWKW YVHDWARAGPEGTT/HPCHFPMAP *TMWPWWQGWRLCMGSAM*TST H*G*PEYSHR*APNLPTAETNTEPSI WHHSSG*STSYLVVG*LYGISSIMER AEVCPHWNRYLLWIWVCLSCMQC FCQDCHLWTHGMPYPPS*YPTQHC L*PRHSLYG*RSAAVGS*SWNSLVL PCFPSS*SSWIDRMVEWPFEVTITVS TR*QYLAGLGQSSPEGRVCSESASNI WYCFSHSQDSQVQESRARSGTTHH HP*GSTSKIFASFSCNITVCWPRGLS SRGRNAATRRHNDSIKLEVKIATQT LWAPPTFKSTG*EGSYSVGWGD*PG L*R*NHSPTP*WR*GRVCMEYRRSI RASLNITMPYD*GQWETTAQARSS
4728	10225	A	5027	2	1284	CHCGPP/VKVEAYGSQVLKGVLAQ VQLTVGPVGPRTHPVVIFPVPECIIGI DMLSSRQNPHTGSLTGRVWTIMVR KAKWKPLELPLPRKIVNQKQYHIPE GIVEISATIKDLKDAGVVIPTTSPFNS PIWPVQKTDGSWRMTVGYCKLNQ VVTPIAAAVPDVVSLLEQINTPPGT WYAAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEINMT

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						KIQGPSTSVKFLGVQWCGACQDIPS KVKDKLLHLVPPTIKKEAQCLVGLF GFWRQHIPHLGMPLQPIYRVTQMA ASFEWGS\EQEKALQQAG\QAAVQA ALPLGP/HKDPADPLVLEVSVSDRD AVWRLWQASI/GHKVGHAQQHSIIK WKWYIRDWARADPEGTTKGQGQR RWWQLAERQDSRDREAAIGERQET AVGKTARDGEAVCD
4729	10226	A	5028	422	1252	TTLFSVQIFQWRQLENLYFREKKFS VEVHDPRRASVTRRTFGHSGIAVHT WYACPALIKSIWAMAISQHQFYLD RKQSKSKIHAARSLSEIAI\DLTRTRT LENSKLANMGSKGKIISGSSGSLLSS GSGARRHCILLPGSQESDSSQSAKK DMLAALKSRQEALEETLRQRLEEL KKLCLREAELTGKLPVEYPLDPGEE PPIVRRRIGP\AFKLDEQKILPKGEEA ELERLEREFAIQSQITEADRRLASDP NVSKKLKKQRKTKYINAVKKLQVY
4730	10227	A	5029	1	400	RHEERTTGILTSEGLASDTSLICVIED FFDTALIISRSSSEGKIQMLDSFLLSL GFLVTEKTVNHLLQQEERPCMDTL DCG/LQVAISEALCRLTIKKSRDELV HKWFDDEVIAEAFKEIKDREFETDS RRFLN
4731	10228	A	5030	1	612	
4732	10229	A	5031	64	323	LFPTLWLLDLLGTVEEILPSLSENIS VWGMKDSVPQGVISLKEKL\STSPD EPVPRSHHVVSLLKSTCLYIFTSG\T TGMIQFFWKA
4733	10230	A	5032	287	508	YYSIFLIYYYYYFLRWSFALVAQAV VQWCDLGSLQPLSPGFKRFS\PSALS SWDYRHEQPRPANFIFLVETGFL
4734	10231	A	5033	1	3627	
4735	10232	A	5034	3	3613	
4736	10233	A	5035	353	406	MLHLQGIIILMIVLYSCCRELIHSFLK DSKSMPNCWGESDGPVTGARHPSW EEEEDGGVWNTTGSQGSASSHNSA SWGQGGKKQMK/CSLKKE
4737	10234	A	5036	1	514	ECKDCGKSFTVSSSLTEHARIHTGE KPYECKQCGKAFTGRSGLTKHMRT HTGEKPYECKDCGKAYNRVYLLNE HVKTHTEEKPFTCTVCRKSFRNSSC LNKHI\HIHTGIKPYECKDCGKTFTV SSSLTEHIRTHTGEKPYECKVCGKA FTTSSHLIVHIRTHTGEKPYICK
4738	10235	A	5037	1	3222	
4739	10236	A	5038	1	4267	MGPWAWKLRWTVALLLAAAGTA VGDRCERNEFQCQDGKCISYKWVC DGSAECQDGSDESQETCLSVTCKSG DFSCGGRVNRCIPQFWRCDGQVDC DNGSDEQGCPPKTCSQDEFRCHDG KCISRQFVCDSDRDCLDGSDEASCP VLTCGPASFQCNSSTCIPQLWACDN DPDCEDGSDEWPQRCRGLYVFQGD SSPCSAFEFHCLSGECIHSSWRCDG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GPDCKDKSDEENCAVATCRPDEFQ CSDGNCIHGSRQCDREYDCKDMSD EVGCVNVTLCEGPNKFKCHSGECIT LDKVCNMARDCRDWSDEPIKECGT NECLDNNGGCSHVCNDLKIGYECL CPDGFQLVAQRRCEDIDECQDPDTC SQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKM TLDRSEYTSLIPNLRNVVALDTEVA SNRIYWSDLSQRMICSTQLDRAHGV SSYDTVISRDIQAPDGLAVDWIHSNI YWTDSVLGTVSVADTKGVKRKTLF RENGSKPRAIVVDPVHGFMYWTD WGTPAKIKKGGLNGVDIYSLVTENI QWPNGITLDLLSGRLYWVDSKLHSI SSIDVNGGNRKTILEDEKRLAHPFSL AVFEDKVFWTDIINEAIFSANRLTGS DVNLLAENLLSPEDMVLFHNLTQP RGVNWCERTTLSNGGCQYLCLPAP QINPHSPKFTCACPDGMLLARDMRS CLTEAEAAVATQETSTVRLKVVPD KTVRWCAVSEHEATKCQSFRDHM KSVIPSDGPSVACVKKASYLDCIRAI AANEADAVTLDAGLVYDAYLAPN NLKPVVAEFYGSKEDPQTFYYAVA VVKKDSGFQMNQLRGKKSCHTGL GRSAGWNIPIGLLYCDLPEPRKPLE KAVANFFSGSCAPCADGTDFPQLC QLCPGCGCSTLNQYFGYSGAFKCL KDGAGDVAFVKHSTIFENLANKAD RDQYELLCLDNTRKPVDEYKDCHL AQVPSHTVVARSMGGKEDLIWELL NQAQEHFGKDKSKEFQLFSSPHGK DLLFKDSAHGFLKVPQRMDAKMY LGYEYVTAIRNLREGTCPEAPTDEC KPVKWCALSHHERLKCDEWSVNS VGKIECVSAETTEDCIAKIMNGEAD AMSLDGGFVYIAGKCGLVPVLAEN YNKSDNCEDTPEAG\YFAVAVVKK SASDLTWDNLKGKKSCHTAVGRTA GWNIPMGLLYNKINHCRFDEFFSEG CAPGSKKDSSLCKL\CMGSGLNLCE PNNKRGDTTGYTGAF\RCLVEKGD VAFC*KHQTVPTGTLGGEKNPDPW A\KDLNEKDY\ELLCLGWVPGKPV\ EEYAN\CHLARAPNHRCGSHGKDK EACVHK\ILRSTASHLFG\SNVTD\CS GNFWLVRS\ETKDLL\FRDDTVC/LW AKLHDRNTYEKYLGEEYVKAVGN LRKCSTSSLLEACTFRRP
4740	10237	A	5039	2	342	LSRVVLSAAATAAPSLRNAA/FLGP GVLQATRTFHTGQPHLVPVPPLPEY GGKVRYGLIPEEFFQFLYPKTGVTG PYVLGTGLILYALSKEIYVISAETFT ALSCSAFELFRDHF
4741	10238	A	5040	53	940	DCYLDVSLTMLSRVV\LSAAATAPT IIMKNAAFLGPGVLQATRTFHT\GQP HLCPMY\PIIPEYG\GKVRYG\LIPE\E

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						FFQFLY/PLKTGVNTDPNVPPETWG LNLVTVLFQRKYMVEFRRRGPSLA LIKY*GGKWVYGNLKKYGSPLVAG LWLD*TPMEQKLGPT*EE/ARQGGF PSQHIQN\AIDYGRSLYQALVQKRH YLF\DVQRNNIAMALEVTYRERLYR VYK\EVKNRLDYHISVQNHDAVRN GTTNSLLNW\VE\KHVRAKLFPPQA RKEDILPKWHCRPIKLLAKEGSKAQ AQLW
4742	10239	A	5041	2	205	APVTSW/IQPKDGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADML\ VSFSGYSSAPKNQEQ
4743	10240	A	5042	1	360	SPCLSERQFCCEKLPLQRSSRPQDSA GQPVT/HAHCSLASTVDLCPPLLAT HRISCWHCQDEVHGGRD\SVDKGD LEALSLPAGHGDTDGPISLDVPDGA PDPQRTKAAIDHLHHKILKSTE
4744	10241	A	5043	106	396	
4745	10242	A	5044	77	4026	
4746	10243	A	5045	1	344	LDFIQTMLQVVGVVSVAVPV/IPWI AIPLVPLGIIFIFLRRYFLETSRDVKR LESTTRSPVFSHLSSSLQGLWTIRAY KAEERCQELFDAHQDLHSGLSISGN GFKGQDLLLFLA
4747	10244	A	5047	3	378	ERDGALTLPLTPGLPSPPPLPP/HTSS QAHYRLSAFGQQFLFNLTANAGFIA PLFTVTLLGTPGVNQTKFYSEEEAE LKHCFYKGYVNTNSEHTAVISLCSG MLGTFRSHDGDYFIEPLQSMDEQE
4748	10245	A	5049	2	278	FVNHGCSQ\TLHFVFKVGNRFQTAR FYRDVLGMKVQAGADRGWRARLE PAPEPALAEGGENGCVVNLSRRVS DLRPCAVFSFRSVASCRWGS
4749	10246	A	5050	1	1539	MRLTPFSLSTGNSFRYSRRLKKNIFG TAPALRVSEMSLRPSSRIFPCFSRNG LDFTIVITLAQPPVPGISFIVAKPRLF PGAGSAGCGLLERLFLSLLLGTGLR WCLRGCFPGARFCSTTSPEGHTTFT GLRRSARTQRLAQGPKPGPPAATV ARQTSRVSPAPPCSLRPGLRHESAPS GIGDVTARGALRGLGCTVRVTAAC GGNHGCSQ/LCLHFVFKVGNRLQT AAFHIGTSMGMKVQQHEEFEEG\CK AA\CNGP\YDG\KWSKTMVG/YLGP EDDHFVAELTYNYG\VGDYKLGN\D FMG\ITLA\SSQAVSNARK\LEWPLT EVAEGVF\ET\EAPGGYKFYLQNRSL PQSDPVLKVTLAVSDLQK\SLNYWC NLLGMKIYEKDEEKQRALLGYAGL TSVSLELQG\VKGGVDHAAAF\GRI\ AFSCPQKE\LPDL\EDLMKRENQKIL TPLVSLDTPGKATVQVVILADPDGH EICFVGDEAFRELSKMDPEGSKLLD DAMAADKSDEWFAKHNKPKASG
4750	10247	A	5051	21	223	HPGSRGCSEPRSGHCTPAWGTKVK T/SRLNKNKTKQKKEVKDCMSSTPL

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						AHPPGVWCEWRGLIPSSSP
4751	10248	B	5052	64	543	RGWKRDREKRDDQDDVSSVRSEG GNIRGSFRGRGRGRGRGRGRGN PRLNFDYSYGYQEHGERTDQPFQTE LNTSMMYYYDDGTGVQVYPVEEA LLKEYIKRQIEYYFSVENLERDFFLR GKMDEQGFLPISLIAGFQRVQALTT NLNLILPPLKDSTE*
4752	10249	A	5053	1	567	AAATSAGA/PGRAVAGAGAGTQRA PGGCPREAPGAAPG\HKARGPGGPF GGEPPPPPPP/LVAVAAVAAGSAGR GRPGR\VAAGPAEKRQPPLLPPKGN PWTKKPPQHLSPDTTGPPPPPLETLE AEFGSLKIIKAGKLKTKKSNKASDF SDMENWPTPSELVNTGFQSVLSQG NKKPPNRKEKEEKGEREEQ
4753	10250	A	5054	3	763	SGRPHPVIRESSPSSSLALGGQLGRG RPSGRAAPGRANPSAPAGGPAREGP EFGSLKIIKAGKLKTKKSNKASDFS DMENWPTPSELVNTWISERPQPRK\ KKPQNRKEKEEKVEKRSNSDSKEN RETKLNGPGENRQ/STDEAQSSNQR KRANKHKWVPLHLDVVRSESQERP GSRNSSRCQPEANKPTHNNRRNDT RSW/ESEIEKKE/HDQDDVSSVRSEG GN\SRGSFRGRGRGRGRGRGRG NPRLNFDYSSC
4754	10251	A	5055	1	372	RHEQGISFLETESTFMTDQLVDALT TWQNKTKVGLLWSA\AHIRFKPTLS QQQKSPEQHETVLDGNLIIRYDVDR AISGGSIQTREALIKILDDLIPRDQFN LIVFSTEATQWRPSLVPASAEN
4755	10252	A	5056	1	1021	AQAQYSAAVAKGKSAGLVKATGR NMEQFQVSVSVAPNAKITFELVYEE LLKRRLGVYELLLKVRPQQLVKHL QMDIHIFEPQGISFLETESTFMTNQL VDALTTWQNKTKAHIRFKPTLSQQ QKSPEQQETVLDGNLIIRYDVDRAIS GGSIQIENGYFVHYFAPEGLTTMPK NVVFVIDKSGSMSGRKIQQTREALI KILDDLSPRDQFNLIVF\STE\ATQWR PSLVPASAENVNKARSFAAGIQALG GTNINDAMLMAVQLLDSSNQEERL PEGSV\SLIILLTDGDPTVGETNPRSI QNNVREAVSGRYSLFCLGFGFDVS YAFLEKLALDNGGLGRG
4756	10253	A	5057	570	831	HGNYRNVCILLGLFYPHFVGEKKIH IGFFLFFPAIDLKSGSGKVYQGPAKG AADTTIILSDEYF\MEVVLGKLDPQK AFFSGRLKAEG
4757	10254	A	5058	1	2229	MGSPLRFDGRVVLVTGAGAGLGRA YALAFAERGALVVVNDLGGDFKG VGKGSLAADKVVEEIRRRGGKAVA NYDSVEEGEKVVKTALDAFGRIDV VVNNAGILRDRSFARISDEDWDIIH RVHLRGSFQVTRAAWEHMKKQKY GRIIMTSSASGIYGNFGQANYSAAK LGLLGLANSLAIEGRKSNIHCNTIAP

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						NAGSRMTQTVMPEDLVEALKPEYV APLVLWLCHESCEENGGLFEVGAG WIGKLRWERTLGAIVRQKNHPMTP EAVKANWKKICDFENASKPQSIQES TGSIIEVLSKIDSEGGVSANHTSRAT STATSGFAGAIGQKLPPFSYAYTELE AIMYALGVGASIKDPKDLKFIYEGS SDFSCLPTFGVIIGQKSMMGGGLAEI PGLSINFAKVLHGEQYLELYKPLPR AGKLKCEAVVADVLDKGSGVVIIM DVYSYSEKELICHNQFSLFLVGSGG FGGKRTSDKVKVAVAIPNRPPDAV LTDTTSLNQAALYRLSGDWNPLHID PNFASLAGFDKPILHGLCTFGFSARR VLQQFADNDVSRFKAIKARFAKPV YPGQTLQTEMWKEGNRIHFQTK\V QETGDIVISNAYVDLAPT\SGTQAKT PSEGGK\LQITFVFEE\IGP\RLKDIGP V\VVK\KVNAVFEWHITKGGNIGAK WTIDLKSGSGKVYQGP\AKGAADT TIH/ILSDEDF/LWEVVLGQA*PSRKA FFSG\RLEGQEGNIMLS\QKLQMIL\K DYAKL
4758	10255	A	5059	1	7449	
4759	10256	A	5060	1	7458	MTDSKPITKSKSEANLIPSQEPFPAS DNSGETPQRNGEGHTL/HQDTQPGR ASLPQRPQR\SGRRRNSLPPSHQKPP RNPLSSSDAAPSPELQANGTGTQGL EATDTNGLSSSARPQGQQAGSPSKE DKKQANIKRQLMTNFILGSFDDYSS DEDSVAGSSRESTRKGSRASLGALS LEAYLTTELLALDFGIFGIRGSLVFA GYPLTLLHTYRQGSNTSSLVFTGLG SGFIELLGCPLRPQQKAAVQRPSMS GLHLVKRGREHKKLDLHRDFTVAS PAEFVTRFGGDRVIEKVLIANNGIA AVKCMRSIRRWAYEMFRNERAIRF VVMVTPEDLKANAEYIKMADHYV PVPGGPNNNNYANVELIVDIAKRIP VQAVWAGWGHASENPKLPELLCK NGVAFLGPPSEAMWALGDKIASTV VAQTLQVPTLPWSGSGLTVEWTED DLQQGKRISVPEDVYDKGCVKDVD EGLEAAERIGFPLMIKASEGGGGKG IRKAESAEDFPILFRQVQSEIPGSPIF LMKLAQHARHLEVQILADQYGNA VSLFGRDCSIQRRHQKIVEEAPATIA PLAIFEFMEQCAIRLAKTVGYVSAG TVEYLYSQDGSFHFLELNPRLQVEH PCTEMIADVNLPAAQLQGFKPSSGT VQELNFRSSKNVWGYFSVAATGGL HEFADSQFGHCFSWGENREEAISN MVVALKELSIRGDFRTTVEYLINLL ETESFQNNDIDTGWLDYLIAEKVQA EKPDIMLGVVCGALNVADAMFRTC MTDFLHSLERGQVLPADSLLNLVD VELIYGGVKYILKVARQSLTMFVLI MNGCHIEIDAHRLNDGGLLLSYNG

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						NSYTTYMKEEVDSYRITIGNKTCVF EKENDPTVLRSPSAGKLTQYTVEDG GHVEAGSSYAEMEVMKMIMTLNV QERGRVKYIKRPGAVLEAGCVVAR LELDDPSKVHPAEPFTGELPAQQTL PILGEKLHQVFHSVLENLTNVMSGF CLPEPVFSIKLKEWVQKLMMTLRH PSLPLLELQEIMTSVAGRIPAPVEKS VRRVMAQYASNITSVLCQFPSQQIA TILDCHAATLQRKADREVFFINTQSI VQLVQSLGTEQDLVFYEKEKRNQSI LGFEPVNSRHVSHVPETHRYKESHY DKCVINLREQFKPDMSQVLDCIFSH AQVAKKNQLVIMLIDELCGPDPSLS DELISILNELTQLSKSEHCKVALRAR QILIASHLPSYELRHNQVESIFLSAID MYGHQFCPENLKKLILSETTIFDVLP TFFYHANKVVCMASLEVYVRRGYI AYELNSLQHRQLPDGTCVVEFQFM LPSSHPNRMTVPISITNPDLLRHSTE LFMDSGFSPLCQRMGAMVAFRRFE DFTRNFDEVISCFANVPKDTPLFSEA RTSLYSEDDCKSLREEPIHILNVSIQ CADHLEDEALVPILRTFVQSKKNIL VDYGLRRITFLIAQEFAEDRIYRHLE PALAFQLELNRMRNFDLTAVPCAN HKMHLYLGAAKVKEGVEVTDHRF FIRAIIRHSDLITKEASFEYLQNEGER LLLEAMDELEVAFNNTSVRTDCNHI FLNFVPTVIMDPFKIEESVRYMVMR YGSRLWKLRVLQAEVKINIRQTTTG SAVPIRLFITNESGYYLDISLYKEVT DSRSGNIMFHSFGNKQGPQHGMLIN TPYVTKDLLQAKRFQAQTLGTTYIY DFPEMFRQASPAAQTRVHVHNVQA LFKLWGSPDKYPKDILTYTELVLDS QGQLVEMNRLPGGNEVGMVAFKM RFKTQEYPEGRDVIVIGNDITFRIGS FGPGEDLLYLRASEMARAEGIPKIY VAANSGARIGMAEEIKHMFHVAW VDPEDPHKKKKTVAFSAGNWIRSL TKVFFKGFKYLYLTPQDYTRISSLN SVHCKHIEEGGESRYMITDIIGKDD GLGVENLRGSGMIAGESSLAYEEIV TISLVTCRAIGIGAYLVRLGQRVIQV ENSHIILTGASALNKVVEPCTVQDIA NHVVSKQVLGREVYTSNNQLGGV QIMHYNGVSHITVPDDFEGVYTILE WLSYMPKDNHSPVPIITPTDPIDREI EFLPSRAPYDPRWMLAGRPHPTLK GTWQSGFFDHGSFKEIMAPWAQTV VTGRARLGGIPVGVIAVETRTVEVA VPADPANLDSEAKIIQQAGQVWFPD SAYKTAQAVKDFNREKLPLMIFAN WRGFSGGMKDMYDQVLKFGAYIV DGLRQYKQPILIYIPPYAELRGGSW VVIDATINPLCIEMYADKESRGGVL EPEGTVEIKFRKKDLIKSMRRIDPAY

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						KKLMEQLGEPDLSDKDRKDLEGRL KAREDLLLPIYHQVAVQFADFHDTP GRMLEKGVISDILEWKTARTFLYW RLRRLLLEDQVKQEILQASGELSHV HIQSMLRRWFVETEGAVKAYLWD NNQVVVQWLEQHWQAGDGPRSTI RENITYLKHDSVLKTIRGLVEENPE VAVDCVIYLSQHISPAERAQVVHLL STMDSPAST
4760	10257	A	5061	6	906	EQPALLPRYRSGIRGYMKTVVLDLL RRYLRVE\TIFSKARDADANTSGMV GGVRSLSFTSVW\VLSPPAHYDKCV INLREQFKPDMSQVLDCIFSHAQVA KKNQLVIMLIDELCGPDPSLSDELISI LNELTQLSKSEHCKVALRARQILIAS HLPSYELRHNQVESIFLSAIDMYGH QFCPENLKKLILSETTIFDVLPTFFY HANKVVCMASLEVYVRRGYIAYEL NSLQHRQLPDGTCVVEFQFMLPSSH PNRMTVPISITNPDLLRHSTELFMDS GFSPLCQRMGAMVAFRRFEDFT
4761	10258	A	5062	2	560	APRLDVSFSQIIHRDIKPENILVSQSG ITKLCDFGFARTLAAPGDIYTDYVA TR*PVDIWALGCMIIEMATGNPYLP SSSDLDLLHKIVLKVGNLSPHLQNIF SKSPIFAGVVLPQVQHPKNARKKYP KLNGLLADIVHAWLQIDPADRISSS DLLHHEYFTRDGFI*KFMPELKA*L LQEAKSQF
4762	10259	A	5063	1	573	
4763	10260	A	5064	2	791	NLVNLIEVFRQKKKIHLVFEFIDHTV LDELQHYCHGLESKRLRKYLFQILR AIDYLHSNNT\VDIWALGCMIIEMA TGNPYLPSSSDLDLLHKIVLKVGNL SPHLQNIFSKSPIFAGVVLPQVQHPK NARKKYPKLNGLLADIVHEIEKEKK PKEIKVRVIKVKGGRGDISEPKKKE YEGGLGQQDANENVHPTSPDTKLV TIEPPNPINPSTNCNGLKENPHCGGS VTMPPINLTNSNLMAANLSSNLFSP QCEVSCNREEP
4764	10261	A	5065	3	524	TYGPASRGICRVSLGRPRWENAAT WKLAAMASIRLQGLHKPVYHALSD CGDHVVIMNTRHIAFSGNKWEQKV YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLQ/NNLHRRTMME RLHLFPDEYIPEDILKNLVEELPQPR KIPKRLDEYTQEEIDAFPRLWTPPED YRL
4765	10262	A	5066	1	250	YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLPKNLHRRTMMER LHLFPDET*RLSAIRE*ELQKITVK*L KLSSDEFL
4766	10263	A	5067	129	796	MGKCSHLANFAAIASIRLQGLHKPV \YHAPE*L/CGDHVVIMNTRHICIF/H GNKWGTKSILFRILAYPGWSLDKVT SLAPAFTLRRSQW/CNL*NLAIYGIP AKKTFTRRTIDWKGLH\LFPDELYS

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						RKIFLKKFS*EELPSTTEKYLNVLDE YTTRRNRRLFKIVDSTLKIIGYKRIRI AENNSEVIETFLLMSFSNLQDGVKQ LLQFEHLFLCAESLWGKVRKV
4767	10264	A	5068	15	350	GPGSAITVGPQPL/RAQRNHRLPVPS PGLSIVMGLRPVPSPGPTGLPGHRQ SSEMRPREAGSLRSSGEKGLPAPVP RPQQSDMTKRTLPRDTPDTPRCPPQ HCPWSRVRGQPQ
4768	10265	A	5069	1	2175	
4769	10266	A	5070	3	86	KNYRGTMS/KTKNGITCQKWSSTSP RRPR
4770	10267	A	5071	2	583	LLLLLFLKSGHGEPLDYYVYAQGA SLFSVTNKHLGAGSTEECASQCVED KEFTCGAFQYHSKEQQCAIMAENK KSSIIIRMRDVVLFEK*MYLSECQTG NGKNYRGTMSKTKNGITCSKMGVP LFPHRPRFSPATHPSEGL\RNPDNDA QGPWCYTTD\PEQRYDYCDIPECEG QEWALGKCFHFCSSPVKINLL
4771	10268	A	5072	844	4515	TVKAPGYSHSHPGALLDLEVGDPN GTNAQLIKCFLLPLCPSFPLCPEECM HCSGENYDGKISKTMSGLECQAWD SQSPHAHGYIPSKFPNKNLKKNYCR NPDRELRPWCFTTDPNKRWELCDIP RCTTPPPSSGPTYQCLKGTGENYRG NVAVTVSGHTCQHWSAQTPHTHN RTPENFPCKNLDENYCRNPDGKRA PWCHTTNSQVRWEYCKIPSCDSSPV STEQLAPTAPPELTPVVQDCYHGDG QSYRGTSSTTTTGKKCQSWSSMTP HRHQKTPENYPNAGLTMNYCRNPD ADKGPWCFTTDPSVRWEYCNLKKC SGTEASVVAPPPVVLLPDVETPSEE DCMFGNGKGYRGKRATTVTGTPC QDWAAQEPHRHSIFTPETNPRAGLE KNATECGGASTELCSTSLCAFTML MDYEGQGEPLDDYVNTQGASLFSV TKKQLGAGSIEECAAKCEEG\EEFTC RAF\QYHSKEQQCVIMAENRKSS\III RMRDVVLFEKKV\YLSECKTGNGK NYRGTMSKTKNGITCQKWSSTSPH\ RPRFSPATHPSEGLEENYCRNPDND PQGPW\CYTT\DPEKRYDY\CDIL\EC *RRECMAFAVGGKLLTGKIFPRTMS WDWECQ\AWGLFRSPHG\HGYIPSK FPNKNLKKNYCRNPDRELRPWCFT TDPNKRWELCDIPRCTTPPPSSGPTY QCLKGTGENYRGNVAVTVSGHTCQ HWSAQTPHTHNRTPENFPCKNLDE NYCRNPDGKRAPWCHTTNSQVRW EYCKIPSCDSSPVSTEQLAPTAPPEL TPVVQDCYHGDGQSYRGTSSTTTT GKKCQSWSSMTPHRHQKTPENYPN AGLTMNYCRNPDADKGPWCFTTDP SVRWEYCNLKKCSGTEASVVAPPP VVLLPDVETPSEEDCMFGNGKGYR GKRATTVTGTPCQDWAAQEPHRHS

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						IFTPETNPRAGLEKNYCRNPDGDVG GPWCYTTNPRKLYDYCDVPQCAAP SFDCGKPQVEPKKCPGRVVGGCVA HPHSWPWQVSLRTRFGMHFCGGTL ISPEWVLTAAHCLEKSPRPSSYKVIL GAHQEVNLEPHVQEIEVSRLFLEPT RKDIALLKLSSPAVITDKVIPACLPS PNYVVADRTECFVTGWGETQGTFG AGLLKEAQLPVIENKVCNRYEFLNG RVQSTELCAGHLAGGTDSCQGDSG GPLVCFEKDKYILQGVTSWGLGCA RPNKPGVYVRVSRFVTWIEGVMRN N
4772	10269	A	5073	9	141	FYRLSLGFKCDWFTMEKRV\KLEER YRDMAEENLKKDISISLKLL
4773	10270	A	5074	3	360	QTKPKESRKRIIMFRT\EFNETENRI ESSSSSSSS\FSSSSSSYKCLARLTK/ RKK/EKIQIIIVRSERKEIITNYRIKRIT KGYYELLYANQLYHLMKCPKFLER HKLLKLTQEETKSGV
4774	10271	A	5076	1	245	AAAYYYYTAARRRQKGERRKKRK EEER\KEEKKKRKKKEKKKRRRG GRRTKKEEKKEKEKKRRTKKEKKK KKKKKKKVVSM
4775	10272	A	5077	68	246	SMAFLTTIEDTALKFIQNHKRPQIA\ KPILSKNRAESITLFNSKIHYMPTVI KPLRVTST
4776	10273	A	5078	3	364	TSIVAAQMFNVITVMQVRISPQHMT SMWPIMVCELSQTFTQLEEDVKDK VESLRSTNKVNRTKVSVTDANGPS VGYIPQSEL\IMYLSACKFLDAALSIP HYKIPLFKIYRWAFIPEVDTE
4777	10274	A	5079	2	1315	GKDAKILCSNPNTGEVLYELPTNTQ RCFDIQWCPRNPAVLSAASFAGRIS VYSIMGGSTDGLRQKQVDKLSSSFG NLDPFGTGQPLPPLQIPQQTAQHSIV LPLKKPPKWIRRPVGASFSFGGKLV TF\ENVRMPSHQGAEQQQQQHHVFI SQVVTEKEFLSRSDQLQQAVQSQGF INYRQKKIDASQTELEKNVWPFLPV TFEDDSRGKYLELLGYRKEDLGK/K DCFGL/GTKWMEPMWLLKTLTKYH ITNHEPAG*PPVTNAAATASSSSTTA KPVFIPTDTSSRWTALPWRTATSWS NRHAPIFFTAQY*RCPRGSYWKYLP ACAVFGNKKNYQETYSR*APHSKD HI*GSYSALPFFSNRPSNQEEAR*CQ QTFGVSV**T*GTDTFTNNHQWFTQ HCKEH*NSKLLRRIDHAYPHS*HQQ LQ*DLCFHASSQSCL
4778	10275	A	5080	18	3600	
4779	10276	A	5081	238	480	SIQFYFFSFQDSKGKHSLVSVIGPQN GWNDPPALNRVPKKKKMPENFMPP VPITSPIMNPLGDPQSQMLQQQPSA\ PVPLS
4780	10277	A	5082	352	4060	DYSRRYILRMKLKEVDRTAMQAW SPAQNHPIYLATGTSAQQLDATFST

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NASLEIFELDLSDPSLDMKSCATFSS SHRYHKLIWGPYKMDSKGDVSGVL IAGGENGNIILYDPSKIIAGDKEVVI AQNDKHTGPVRALDVNIFQTNLVA SGANESEIYIWDLNNFATPMTPGAK TQPPEDISCIAWNRQVQHILASASPS GRATVWDLRKNEPIIKVSDHSNRM HCSGLAWHPDVATQMVLASEDDR LPVIQMWDLRFASSPLRVLENHAR GILAIAWSMADPELLLSCGKDAKIL CSNPNTGEVLYELPTNTQWCFDIQ WCPRNPAVLSAASFDGRISVYSIMG GSTDGLRQKQVDKLSSSFGNLDPFG TGQPLPPLQIPQQTAQHSIVLPLKKP PKWIRRPVGASFSFGGKLVTFENVR MPSHQGAEQQQQQHHVFISQVVTE KEFLSRSDQLQQAVQSQGFINYCQK KIDASQTEFEKNVWSFLKVNFEDDS RGKYLELLGYRKEDLGKKIALALN KVDGANVALKDSDQVAQSDGEESP AAEEQLLGEHIKEEKEESEFLPSSGG TFNISVSGDIDGLITQALLTGNFESA VDLCLHDNRMADAIILAIAGGQELL ARTQKKYFAKSQSKITRLITAVVMK NWKEIVESCDLKNWREALAAVLTY AKPDEFSALCDLLGTRLENEGDSLL QTQACLCYICAGNVEKLVACWTKA QDGSHPLSLQDLIEKVVILRKAVQL TQAMDTSTVGVLLAAKMSQYANL LAAQGSIAAALAFLPDNTNQPNIMQ LRDRLCRAQGEPVAGHESPKIPYEK QQLPKGRPGPVAGHHQMPRVQTQ QYYPHGENPPPPGFIMHGNVNPNA AGQLPTSPGHMHTQVPPYPQPQPY QPAQPYPFGTGGSAMYRPQQPVAP PTSNAYPNTPYISSASSYTGQSQLYA AQHQASSPTSSPATSFPPPPSSGASF QHGGPGAPPSSSAYALPPGTTGTLP AASELPASQRTGPQNG\WNDPPALD \KVPKKKKMPENF\MPPVPITSPIMN RLGDPQSQMLQQQP\SAPVPLSSQSS FPQPHLPGG\QPFPWGYSKPFGFKQ GMATIFFQSPNIEGAPGAPIG\NTFQ HVQS\LPTKKITKKPI\PD\EHLILKTT FEDLIQRCLSSATDPQTKRKLDDAS KRLEFLYDKLR\DRTFSPTITSGLHNI ARSIETRNYSEGLTMHTHIVSTSNFS ETSAFMPVLKVVLTQANKLGV
4781	10278	A	5084	121	419	DLCFTTPKAGRRQEITKIRAELNKV EVQETIQKISEKRSWLFNIINKIARLL TRLIQKKD\QINTVRNDKGDITTYPT EIQKTLRDYYEHLYACRVENLQ
4782	10279	A	5085	1	279	TMDSNNTV\DQLDL\TDIYRTLHLTS AAYTFFSSAHRLCSRI\DLRLSHKTS LNKFKKIVIIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4783	10280	A	5086	1	279	TMDSNNTV\DQLDL\TDIYRTLHLTS AAYTFFSSAHRLCSRI\DLRLSHKTS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LNKFKKIVIIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4784	10281	A	5087	1	1915	MAILPLLLCLLPLAPASSPPQSATPS PCPRRCRCQTQSLPLSVLCPGAGLL FVPPSL\DRRAAELRLADNFIASVRR RDLANMTGLLHLSLSRNTIRHVAA GAFADLRALRALHLDGNRLTSLGE GQLRGLVNLRHLILSNNQLAALAA GALDDCAETLEDLDLSYNNLEQLP WEALGRLG\NVNTLGLDHNLLASV PAGAFSP\LHKLARLDMTSNRLTTIP PDPLFSRLPLLARPRGSPASALVLAF GGNPLHCNCELVWLRRLAREDDLE ACASPPALGGRYFWAVGEEEFVCE PPVVTHRSPPLAVPAGRPAALRCRA VGDPEPRVRWVSPQGRLLGNSSRA RAFPNGTLELLVTEPGDGGIFTCIAA NAAGEATAAVELTVGPPPPPQLANS TSCDPP/PGRGLPDALTPPSAASASA KVADTGPPTDRGVQV\TEHGATAA LVQWPDQRPIPGIRMYQIQY\NSSA DDILVYRMIPAESRSFLLTDLASGRT YDLCVLAVYEDSATGLTATRPVGC ARFSTEP\SLRPCGAPHAPFLGGTMII ALGGVIVASVLVFIFVLLMRYKVHG GQPPGKAKIPAPVSSVCSQTN\GAL GPTPTPAPPAPEPAALRAHTVVQLD CRALGARPRTCGTLARRPPL
4785	10282	A	5088	1387	1567	GKNLLPLFFFFFFFETVSQSVAQAG VQWRHLGSPKPLPP\GSSDSPASVSQ AAETTGTCHH
4786	10283	A	5089	96	408	SPRKRKTRHSTNPPLECHVGWVMD SRDHGPGTSSVSTSNASPSEGAPLA GRYGCTPH\SFPKFQNPSHELLKEN GFTQQVYHKYRRRCLSERKRLGIG QSQEMNT
4787	10284	A	5090	390	665	PLNIHYCFLGGKYLVFGFSVAANKT SGAP\GNSPVSAIRAFGDAHPDLVT\ PGTF\IPYCSMAHAQLCFHGHRDAV KFFVAVPGQVISPQSSSS
4788	10285	A	5091	185	386	WEASKKKPRGAQISNAITTYKYLPK VGV\KNYQTEALYKPIQTGKIGHPV FFQKPPLLGDGQNYDTPP
4789	10286	A	5093	3	330	GTGLKARKSASSLPETFPTRTRHGE AALPLSPTWKMTGPVGNPMIPRQR SMSLLTAVSGQPHFQDSALSQASSS PDLL/LHLSPR\SCPGRVQETLKATD RPPRCPAGCG
4790	10287	A	5094	2	349	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLKKGENPPNSFYGAIIP RIPNPNMDLPSSSPT/RPVSGRNMEA KIFTKFLAGHFKQSFGREIHHDQREF IPGIQGGFNIGN
4791	10288	A	5095	2	353	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLASSSSSSSSSSSSSSSSS SSPPNMDLPSSSPT/RPVSGRNIEAKI FTKFLPGHFQQSFGRVTHLDQRELI LGNQGGSTICKS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4792	10289	A	5096	1	262	RGRAGGEPLPATTGAAPPPGRRLH/ RQLPDRRGLASMPREEKASLNEPG GPGRGRRRGSVQLHGEGGPRGGEE GTGREEWNEKAEFTL
4793	10290	A	5097	116	177	LGEHGVYSGVGTGGRLSS*KKGKP WFK*KKLKGGPIPI*RDPRGFSRFSV
4794	10291	C	5098	231	347	MGLGPHLKFFYLKHGLPFFKELNPL KVKIWPRNPWIKKI*
4795	10292	A	5099	518	931	ATRHSMLSCIIYTYIYIKHTHTHVFI YIYTYTYIHTHIYTYTYICIHTHIHIYI YIYIHTHFFFFFFFFFETESRSVTQAGV QWHDLGSLQAASWGHA/DSPASTS QAAGTTGAHHHAQ/LIFFFFVFLVET GPHRASQDS
4796	10293	A	5100	2	1109	DAEMLVMAPRTVLLLLSAALALTE TWAGSHSMRYFDTAMSRPGRGEPR FISVGYVDDTQFVRFDSDAASPREE PRAPWIEQEGPEYWDRNTQIFKTNT QTDRESLRNLRGYYNQSEAGSHTL QSMYGCDVGPDGRLLRGHNQYAY DGKDYIALNEDLRSWTAADTAAQI TQRKWEAARVAEQDRAYLEGTCV EWLRRYLENGKDTLERADPPKTHV THHPISDHEATLRCWALGFYPAEIT LTWQRDGEDQTQDTELVETRPAGD RTFQKWAAVVVPSGEEQRYTCHVQ HEGLPKPLTLRWEPSSQSTVPIVGIV AGLAVLVVTVAVVAAVMCRR KSSGGKGGSYSQAASSDSAQGSDV SLTA*KA
4797	10294	A	5101	3	1145	SDSPQTPRMRVMAPRTLILLLSGAL ALTETWACSHSMRYFYTAVSRPGR GEPRFIAVGYVDDTQFVRFDSDAAS PRGEPRAP\WVEQEGPEYWDRETQ KYKRQAQTDRVSLRNLRGYYNQSE AGSHTLQWMYGCDLGPDGRLLRG YDQSAYDGKDYIALNEHLRSCTAA DTAAQITQRKWEAARAAEQQRAYL EGTCVEWLRRYLENGKETLQRAEH PKTHVTHHLVSDHEATLRCWALGF YPAEITLTWQRDGEDQTQDTELVET RPAGDGTFQKWAAVVVPSGEEQRY TCHVQHEGLPEPLTLRWEPSSQPTIP IVGIVSGPAVLAVLAVLAVLGA VVAAVIHRRKSSGGKGGSCSQAAS SNSAQGSDESLIACKA
4798	10295	A	5102	3	242	GFWAPRVCKDIDKWHLSEPEALWF GEGGSPGGCRW\GGWLCQGKNRA AGGVGAEGACLGLLSATGLLWMT GLQEPREPQV
4799	10296	A	5103	1	138	FPLIPKPGKDPFN/ENFRPIFLMAKN AKILKKILANLIFQPLKKIL
4800	10297	A	5104	59	337	IPYPALPFTSVEAPNSHVKAVMKTS VLLSWEIPENYNSAMPFKILYDDGK MVEEVDGRATQKLIVIL\NPEKSYSF ELTYRGNCAGGLELMVT
4801	10298	A	5105	54	226	TKAETENLNRPVT/EIKSVI/NSLPTK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KSPGLDGFIAKFFQTYKREIIPTLLK LLQKLKW
4802	10299	A	5106	2	265	ETVKLLEENI/GQKLFDIGLGSDFLDI TPKAQETKINKWDFIKLKSFCTVKE TIKMKRQSVEWEKILVSHVSDKWFI SKIQGIYITQYQ
4803	10300	A	5107	1	296	GREKEEGESGEDWGRV\GREKEGG EGREEEGEGGREEEGEGGRKEEGE GGREEEGEGGREEEGEGGREEEGE/ GREEEGEGGRQEEGEGGRRREGRG GRS
4804	10301	A	5108	1	253	
4805	10302	A	5109	190	472	
4806	10303	A	5110	1	314	HNVVPHVFMLQKEITKKNSTFRVHI KAVFYN/HDIYCMPPLLNYRKTFDV IVIDPPWQSKSVKRSNRYSYLSPLQI KQIPIPKLAAPNCLLVTWLTNTQKH LRFIK
4807	10304	A	5111	3	362	FFFFFETESLSVPQAGVQ*HDLSSLQ PP/PPGFTPFSCLSLPSSWDYRCPPPR PA/NIFFVFLVETGFHHVSQDGLDLL T/S/GDPPASASQSAGITGVSHRARPP PPQFFIQLPLYNIHTLEGR
4808	10305	A	5112	3	385	FFFETESRSVAQAGGQWHDLSSLQ APTPGFTPFSCLSLPSSWDYRCPPPC PANFFVFLVETGFHHVSRDGLDFLT S\DPPTSASQSVGITGVSHCARARPF FKKKKKKKTSILSSSSLFSHKQRSFG F
4809	10306	A	5113	1	390	SKAVKV/YRLITRNSYEREMFDKAS LKLGLDKAVLQSMSGRDGNITGIQ QFSKKEIEDVLRKGAYAAIMEEDDE GSKFCEEDIDQILLRRTTTITIESEGK GSTFAKASFVASGNRTDISLDDPNF WQKWA
4810	10307	A	5114	2	214	GRVDIERAIILVQTGQQALEPA\VRL RRAPYPCHTSDLFLNNVGFFFPLIM MLTWMVSVASMVRPLVSQQE
4811	10308	A	5115	30	379	KRSVNSPGRALSELCVSTELGFLRC VSVVCSLSQEYFLFTTLLYFGL/LPF ACLLSSSPVFFVFRCSVPLFFCFLFC VSLCLPFLGFFHVLFFHRLLPIVFSF MEGFYWAWCLVFFCL
4812	10309	A	5116	1	304	GTRETVGLGDTNLAHQCSRLTMVN NDNHSEAYNNLAVLEMRKGHVQQ ARALLQTASALSPHMYET\DFNFATI CDMTGYLHRSYVDAQKSEAALSEH VDTQH
4813	10310	A	5117	119	264	
4814	10311	A	5118	720	2798	VYWPHSFLGCPSNYPLYLGAETRQ GGRARPPFLPLSFPPRFPRPNSPFQN VLETQRISYSFPLLADTSNTRATSGH AQQPAPILPLREVAGAEDIIRVHVPF SLSDLSQIAKRLGSFSSDPDTYIKEF KYLTQSYELTWHDLYIILSSTLLPEK KERVWLAAQAHANDLHRQDPTKPI GAAAVPLEEPPWKYQPTDPGRASR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NHMITCLIAGLNKAAHKAVNFEKL KEISQRADENPAEFLSRFTEALQKY TRVDPTSREETIVLNNHFISQSAPNI QHKLKKAEDGPQTPQQDLLNLTFK VFNNREEQIKLDKAQRDCAKYQLL AVAIHQPSHSTQGHKKPNGSNPPGP CFKCSKEVTYLGVQLSPGAQAMTP AQATLINSLPLPSSKNEILSFLRLEGF FRIWIPNFALLAQPLYEAAKGPLNE PLSPIHNILPSFCKLQTALITAPALSL PDLSQPFVLYTTKNQGIALGVLGQQ KGNPPSFDPVAYLCKQLDNTVKGQ PTCLKASSAVAVLPLESKKLTFGQS TTIHSPHNLQDLLSSWALSSLSPSQI QSLYALFIKNPEFSLAKSAPLNLASL LPISSSPPTHSCTDILDHLQPQFPNISS KPLTNPDDQLFIDDSSSRAPGSPKIV GYAVVTLNHVIEAKPLPPETSSQKA EL\ALTRALTLSKDKQHWLISEPVQ RPPPSSVHST
4815	10312	A	5119	2	697	HGRLLLLLLLLLLPCCEKTTEGEAM KEITAGLPVKVV\VDVLRQASKACV VKREFKKAEQLIKHAVYLARDHFG SKHPKYSDTLLDYGFYLLNVDNICQ SVAIYQAALDIRQSVFGGKNIHVAT AHEDLAYSSYVHQYSSGKFDNALF HAERAIGIITHILPEDHLLL\ASSKRV KALILEEIAIDCHNKETEQRLLQEAH \DVHLSSLHLASKSYGDLAVVVLVH MSLLKSY
4816	10313	A	5120	3	277	EEEAAPPPGRERARGKGGDRPRGG NPEHQCGGTPRAEGSSTA/A/PPTCT SSSRTPASTVGPEPCGAGSAATAPG PELSGQNQMGRGPPVEDTE
4817	10314	A	5121	1	337	GTSSCVREVVQAMGKKKVLVKVH LKDKFVIDVDKNISISDVTPSSLVVL RNDSYTLHKILPNKVHSLVSLMMV NTVPY/STNETIVSLDGPMVTILFSD KLSFTAPQLYIFTG
4818	10315	A	5122	2	302	ARGLPFFTRNDFSVWTIA/RNKCVG LELSKITMPIAFIQPLIFLHRITEYME HVYLIHRAFCQPQPLERMQVGLKG ARQEFVMKVMPLACLATQSWGPR HL
4819	10316	A	5123	3	346	HENWKKLLPCSSKAGLSVLLKADR LFHTSYHSQAVHIRPVCRNARCTSIS WELRQTLSVVFDAFITGQGKKDWS LF/RMFSRTLTEPCPLASESRVYVDI TTYNQDNETLEVHPPP
4820	10317	A	5124	213	425	QNSQGKLFSSGCLPFCGSNTKGIILK YIQNH/KKPQIAKATLSKKNKAGSIT LPDFKIYYKALKPKITWYWH
4821	10318	A	5125	1	356	GTSTRIIFYRDGVSEGQRQQGLHHE MLAIREACIKLQKDYQPGITFIVVH NIHHTRLLCSDKNHPLGKRGNSPTG SNCGTKITHPTEFDFYLRRHAGIQG TSRPSYYHVLWD\DNRFFS
4822	10319	A	5126	1	238	HMHSHHMHSHTPHA/HHTHHMHS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HHMHSHTHHMHSHHMHSHAPHAL TPHACTHTHHMHSHHMHSHHMHA LTPHACTHTPH
4823	10320	A	5127	180	405	IWGEQDTFHSMAKWIIHLNVNHKT VKLLDDNIG/IKRGDLG/VDNEFLGT TPKAQSMEETIDKLDFIKMKNFCSV KDG
4824	10321	A	5128	61	85	PS*NYPP*KGITFGPLNKK
4825	10322	A	5129	3	2004	RRRRRPASPPAGLALAPRSPSASPEP REGETLSPSMQREEGFNTKMADGP DEYDTEAGCVPLLHPEEIKPQSHYN HGYGEPLGRKTHIDDYSTWDIVKA TQYGIYERCRELVEAGYDVRQPDK ENVTLLHWAAINNRIDLVKYYISKG AIVDQLGGDLNSTPLHWATRQGHL SMVVQLMKYGADPSLIDGEGCSCI HLAAQFGHTSIVAYLIAKGQDVDM MDQNGMTPLMWAAYRTHSVDPTR LLLTFNVSVNLGDKYHKNTALHWA VLAGNT\TVISLLLEAGANVDAQNI KGESAPDLAKQRKIVWIINHLQEAR PAKGYDNPSLPRKLKADKEFRQKV MLGTPFLVIWLVGFIADLNIDSWLI KGLMYGGVWATVQFLSKSFFDHS MHSALPLGIYLATKFWMYVTWFF WFWNDLNFLFIHLPFLANSVALFYN FGKSWKSDPGIIKATEEQKKKTIVE LAETGSLDLSIFCSTCLIRKPVRSKH CGVCNRCIAKFDHHCPWVGNCVG AGNHRYFMGYLFFLLFMICWMIYG CISYWGLHCETTYTKDGFWTYITQI ATCSPWMFWMFLNSVFHFMWVAV LLMCQMYQISCLGITTNERMNARR YKHFKVTTTSIESPFNHGCVRNIIDF FEFRCCGLFRPVIVDWTRQYTIEYD QISGSGYQLV
4826	10323	A	5130	3	144	HEKYHKN\TALHWAVLAGNTTVIS LLLEAGANVDAQNIKAILRCHMAL
4827	10324	A	5131	148	325	RQGKECKIHCKKKLSPGIRSYPVEN/ F/VDTMYDYLQPAYYKLNDLTNAD PCAVRYLLFDQN
4828	10325	A	5132	175	405	NILNSQFSTFLNDYVEFFVVFKIFNFI IIIF*DRVSICCPGWSIMVQSWLTAA LTFGRR*SSNLSLPSSWDYRRVP
4829	10326	A	5133	14	26	YSPHEVGWKGRNREKMFCSEINVV FPDSVCQEMGFHHVAPAGLELMSS SDSPASASQSAGITSVSHHSCLYTSK GVE*FTGIIFSS
4830	10327	A	5134	177	454	PLLERAKIGPRPEKPMETRQGWGPF SPKVPGQKKFWG*LAPIPSPGMHPN PILGPMV*EGGP*PPGILGPP*PYGKP LF*RKRGSNGGPYLQ
4831	10328	A	5135	3	92	NAWRTATEEWWTEDWNEDCSEP* HFTYVI
4832	10329	A	5136	1	442	PLIMNSIKSFSDHAQCGR\EFDRQED DIHLVTLCVTELNDREENENHFPVI YGIAVNIKTAEIYRASFQDRGPEEQL

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RAARTLAGGPMISIYDAETEQLRI\G PYSWTPFPHVDFW\LHQDDKQIFEN LSTSPLAEPPHFVEHIRSYLD
4833	10330	A	5137	177	566	EPFWSLSYLSLRRGGRNVRLCRLSA LVFCQFKAMLLTLTAGNNKTAEIY RASFQDRGPEEQLRAARTLAGGPMI SIYDAKTEQLRIGPYSWTPFPHVDF WLHQNDKQILKGRVYRLGKS*ISAP WFPHL
4834	10331	A	5138	1	981	PLLVEGR*VRLPQSAGDLVRAHPPL EERARLLRGQSVQQVGPQGLLYVQ QRELAVTSPKDGSISILGSDDATTCH IVVLRHTGNGATCLTHCDGTDTKA EVPLIMNSIKSFSDHAQCGRLEVHL VGGFSD\DRQLSQKST\HHFLIEFDR QEDDIHLVTLCVTELNDREENEN\H FPVIYGI/AVILLSLTAVNIKTAEIYR\ ASFQRSGVREEQA/LRAARKL*AGG PMIS\IYDAETETTS**DPYFLGHPFP HVGF\WL\HQD\DKQILDESFHFRPL AE\PPHF\VEHIRSTLMVF*KNTPSPA \NTLFPGNKALLYKKNEDGLWEKIS SPGS
4835	10332	A	5139	1	405	AYVTVCNQCGRESKLLSKFYELEL NIQGHKQLTDCISEFLKEEKL*GDN RYFCENCQSKQNATRKIRLLSLPCT LNLQLMRFVFDRQTGHTKKLNTYI GFSEILDMEPYVEHKVW*PTSLNSM LSLKLGGMCMLT
4836	10333	A	5142	2	204	ETGFCHVVQAGLKLLGSSDLPASAP QSAGITGMCHCAQPTKVSVASKVF KGSHKD*ILT*GYANKGA
4837	10334	A	5143	1	360	QQLTVLVAHLGVTLMDQRGYHWL LKSLMTQYQGLLYENP*ITLEIVNTL NPGTLLPNESVPGSALHCRVDVVHE MLSIQRDLTDHTLRDSDIEYFIDRSG FILGGDPLSGVCSSDFGLST
4838	10335	A	5144	36	380	FVALMGHKMSHNKFKIEIIRSMFSN HNRSQ*SK*IKEIYKCGN*HTSK**M H*GKKSLAKLENNEMNENESTT*Q NLWDAAKTALNEQFML*MPILKKG *MSQINKPTFHLKTIK
4839	10336	A	5145	1	362	ELNLPAPELPRKRTENLFLQLAEYV AHSLNVTS*YVCEGTTMGD*WPWE TQELEPTDPVPDIIPVQKAQTSNFW VLKTSINGQYCIPRKGKDFTIPVGRL N*LGQKLYKSITGTQGQSPG
4840	10337	A	5146	2	428	MFLLVVINLHILFVF*FKLFSWS*AIF L*FLF*FMSESENIYYAEIGIIITIVVT LKSLIIATYCINPSSHCYKVYLVLSY LYCIIVNFDIYFLLLCVPFCYFSLIISL SPLFLLIYMIFLYIHFILLLFVIFYTFIP FSFY
4841	10338	A	5147	3	361	TLFQL*DLRKQRLEDLSTLIPRIYPG WKCRTHFLLMKKSQIVIAGWYRRY AQHKRNQPTKSTVLVLQSYIRGRK ARKILRELKHQKRCTEAVTTIAAY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WHGTHALTETERLKEEARRKH
4842	10339	A	5148	1	424	VHLTADDKVIIAGLWSIVNAQDAV GETLGRLQGVYPWIQRFFGSFGNLS SASAIVVNPKVTAHGKNVLTSLVD AITHLVDLMGTFAQLRELH*DKLYE DPENLHTLGHVLVTVLVIHFGT*FT AEVQASWLMMDTERANAL
4843	10340	A	5149	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
4844	10341	A	5150	38	501	APSPDA\MGHFTEEDKATI\TSLWGK \VNVE\DAGGETLGRLLVVYPWTQR FFD\SFGNLSSASAI\MGNP\KVKAH GKKVLT\SLGDAIKHLD\DLKG\TFA QA*SELH\CDK\LHVDPENFKAPGG NVAGDPFLAIPFSAKEFHPLKVARL SWAERWVTW
4845	10342	A	5151	2	198	KVRPPPLKKTFDSVDYRVLSEVDFE ERFAELPEFRPEDDLSSFS*PFLSPPP CMSTALAHGDFSL
4846	10343	A	5152	1	119	DIMTGPHDEVAAKNIQLTNEIQTLE TE*HEATKEFQVLS
4847	10344	A	5153	3	83	RMVLRLMPLSTDEALCFHAMFQPF LDMIHEAQQAMDIHFHSPDFQHPPT EFIREGDDDRTVLREMHHI*TG*LR VKWRCEEWR*I
4848	10345	A	5154	2	370	GAARLDERTKEGSDDEDSG*GARA ELEGNKEGESEGQYKAKGERSAWS KLRTEIRQKAEESIDGIKVDDPS*IS MKATYTTMKIS*RQIRKIRQREKKN TAKGEGQERQNKNLSHKRHDISC
4849	10346	A	5155	106	344	RPCQQMQINVIHPINRMDKKHVIIPI DTSDKI*HPFMIQTLNTLCI**MYLSI IKAIYDPYTADIILTG*TFNAFFSTI
4850	10347	A	5156	198	474	
4851	10348	A	5157	1	131	PQEVPQSFGPPGDKAGC*GAGKMS PRERGGFLKCAEGGHPAPA
4852	10349	A	5158	104	440	FSKIYHFLLCCCFVLSKNCPILLHFL KIYLLALGNINISYFYSYHSKTLATG LKLTDDSQHISHGTSGSRFKCLLLS KAVLMSSLPAVYS*LLKLLDVREVS NMVHDTLGIL
4853	10350	A	5159	2	393	EVWPRGLMGYVTVTEPSAVLVVRG VRDRLVITYPHEHHALTSSRLYLLM LFVGDPSGSGSNGSPDS*GLLLFRN DQAHIDLFVCFSVILSCFFLFLSLCEL LWNAKQAMDQRQEQRRHLQEMTK MARRPF
4854	10351	A	5160	2	154	FRDGVSLHCSGWS*TPGLK*SSCLS LPKCWDYRHEPPLLFPLWRAIGNIY
4855	10352	A	5161	142	399	HLLTYSEMFLGGVRYFLQSTLPADL SKHAYLYAP*LRLFA*RYTSAFTEW THSANKTVCLMPKLYELTYVGIDTL ATPVIKRYYCS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4856	10353	A	5162	3	410	HEG*PTFSSILHPHPGAWAQLQ*PSQ ATTALFTLISVA*QQAGCSPQPGAG NTPPPPPNSGTLTPSPACAHWAQC* ANKDEFSVPGPQCLWPR*GPSYTAS LPQALRARPSQMTRVPQAPPPTGPG PVVSPCANTN
4857	10354	A	5163	168	435	IIAQ*N*FLKNNFQ*TI*K*NKTILFTT RSK**I*QKQQKNLYLEKYKTLLKEI KDLNKWKNISCSWIGTLSIDKLVTL SKLNYRVNVI
4858	10355	A	5164	2	427	QIFRYLIMEKEQEHTYRGFKTVNR WTDAYDYAQHYSEASVASKDVSV W*FHDYLGMSRHPDVLQA*QETLQ RHGAGSGGSRNLSGTRNCHVELEH ELADLHLKDSSLIFSFCFIANDCTLF TLAKILPGREIHSDACQHAFM
4859	10356	A	5165	11	1232	MAGAATGSRTPGRSELVEGCGWRC PEHGDRVAELFCRRCRRCVCALCP VLGAHRGHPVGLALEAAVHVQKLS QECLKQLAIKKQQHIDNITQIEDATE KLKANAESSKTWLKGKFTELRLLL DEEEALAKKFIDKNTQLTLQVYREQ ADSCREQLDIMNDLSNRVWSISQEP DPVQRLQAYTATEQEMQQQMSLG ELCHPVPLSFEPVKSFFKGLVEAVES TLQTPLDIRLKESINCQLSDPSSTKP GTLLKTSPSPERSLLLKYARTPTLDP DTMHARLR\MSADRLTVRCGLLGS\ LGPVPVLRFDALWQVLARDCFATG RHY\WEVDVQEAGAGWWVGAAY ASLRRRGASAAARLGCNRQSWCLK RYDLEYWAFHDGQRSACGPATTST GSASSWTTRPASSPSTT
4860	10357	A	5166	115	447	MSSWARLCESPVVWYF*HVLFVCL HKLRALISQQFLTGINCQLSDPSSTK PGTLLKTSPSPERSLLLKCKTPGSGD RVETVEMVGCWVEEDHGNGGPSFF LIRIYLFIYLF
4861	10358	A	5167	1	423	ADMKAHHLLHSGGMGFSCECSTGF VKHS*LIEHIRTHTGEKPFQCPKCDK SFRLKAQLLSHHGLLTGDRPFHCPE CDKNLRERGHMLRHQRIHRPERPF ACGYCGKGFIYKSKLAEHIRVHTKS CPAANELDIKKMLHPLV
4862	10359	A	5168	481	908	EGSQWEAQKALAIQPVPCGAVRVP WTTSISSPASIPKQSVGKGCDCLR*L GDFAPARGEEACECHTEPFRNSRGV GGAWARPGYLVLSLLSLQCPDSAC NQDLLAYLQRIALYCHQLNICSKVK AEVQNLGGELVVSGVSIS
4863	10360	A	5169	2	2799	EMTAVHAGNINFKWDPKSLEIRTLA VERLLEPLVTQVTTLVNTNSKGPSN KKRGRSKKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVVAVEDV RKQGDLMKAAAGEFADDPCSSVKR GNMVRAAPALLSAVTRLLILADMA DVYKLLVQLKVVEDGILKLRNAGN EQDLGNQYKALKPEVDKLNIMAAK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RQQELKDVGHRDQMAAARGILQSN VPILYTASQACLQHPDVAAYKANR DLIYKQLQQAVTGISNAAQATASD DASQHQGGGGGELAYALNNFDKQI IVDPLSFSEERFRPSLEERLESIISGA ALMADSSCTRDDRRERIVAECNAV RQACRTCVSEYMGNAGRKERSDAL NSAIDKMTKKTRDLRRQLRKAVMD HVSDSFLETNVPLLVLIEAAKNGNE KEVKEYAQVFREHANKLIEVANLA CSISNNEEGVKLVRMSASQLEAGCP QVINAATWALAPKPQSKLAQENMD LFKEQWEKQVRVLTDAVDDITSIDD FLAVSENHILEDVNKCVIALQEKDV DGLDRTAGAIRGRAARVIHVVTSE MDNYEPGVYTEKVLEATKLLSNTV MPRFTEQVEAAVEALSSDPAQPMD ENEFIDASRLVYDGIRDIRKAVLMIR TPEELDDSDFETEDFDVRSETSVQT EDDQLIAGQSARAIMAQLPQEQKA KIREQVASFQEEKSKLDAEVSKWD DSGNDIIVLAKQ\MCMIMMEMTDFT RGKGPLKNTSDVISAAKKIAEAGSR MDKLGRTIADHCPDSACKQGLV\A YLQGIALYCHQLNICSKVKAEVQNL GGELVVSGNCDTCGALQGLKGWPP PLCLATHWVDSAMSLIQAAKNLMN AVVQTVKASYVASTKYQKSQGMA SLNLPAVSMKMKAPEKKPLVKREK QDETQTKIKRASQKKHVNPVQALS EFKAMDSI
4864	10361	A	5170	25	458	
4865	10362	A	5171	3	764	GPLCIALALQEFGTRRRWACRSLSS SGRRSLFRRMGSVKAVKNKAYFKR YQVKFRRR\RKGKTDYYAR*RLVIQ DKNKYNTPRYRMIV\RVTNRDIICQI AYARIEGDMIVCATYAH*LPKYGV KVGLTNYAAAYCTGLLLARRLLNR F\GMDKIYEGQVEVTGDEYNVESID GQPGAFTCYLDAGLARTTTGNKVF GALKGAVDGGLSIPRSTKRFPGYDS ESKEFNAEVHRKHIMGQNVADYM RYLMQEDEDAS
4866	10363	A	5172	8	400	PLASFDTGDVECALCMRLFYEPDTT PCGHTLCLRCL*RCLYHNAKCPLCK DGLSQ**ASIKYSYNVIVEELIAKFL PEELKEREKLYE*EMEELYNLNNNV PILMCTMAYANVTCPLHMFEPCYR LMIRIW
4867	10364	A	5173	2	400	SLPLASFNTCNVECALCMRLFYEPV TTPCGHTFCLKCLERCLDHNAKCPL CKDGLSQCLASRKYIKNVIMEELIA KFLPE*LNERMKLYEYEMEELSNLN NNVPIFVCTMAYPTDPCPLHIFEPCY RLMIRIC
4868	10365	A	5174	1	216	AGRTGRPEERAPESKSGSGSESEPSS RGGSLRRGGEACGTSDGGPSPF*GS SVVSFTLLSYLGYYSYLLSTV

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4869	10366	A	5175	301	446	SYFSYIILIIRGNESEGGFFEN*YFCL LINGGSWSGEPPRRNSHTFNC
4870	10367	A	5176	155	404	AAVPSRILKQYSHPNIVRLIGVCTQK QPIYIVMELVQGERGALSSR*GAQP GQVAALPQEAQQGSSPPAGGDFLTF LRTEGAR
4871	10368	A	5177	172	443	TGMIRGPWTKVGPGAIEKPPVGDK VPNGCPKSLGNRQPCF*VLEVNEPY VPKKFKAEPFPFHANICPLSEKERQF RKQTALVDL*KPKPR
4872	10369	A	5178	3	428	PDQTLLCCCAEMGSHCVAQAGLEL LGLSDLPILASQSAAITGVGHHACP VLGS*RPSQMLCPFPWWLLLSATFY LAVPHLLPCLLFQPHSLRCSRSSSSA NLPVVFSPGAGCLSLLSCMECSSFP AKVLVIPFPSERPPCS
4873	10370	A	5179	2	432	NIVSQNNDLPQTVIWMGDCIISLETR IQMQCDWNTSDFCVTPHS*NETEH HWEIKCHLVGREENLTLDIVKVKE QVFEASQAHLTLLPGTDIFSEAANG LSAINSLKWIKTTGNSTLVNFVLIIIC LFLAAAFSPEAASASVD
4874	10371	A	5180	163	585	VEVRAHPKKRQRKKKEKKKSDRYS SSSSSSSDSSSSSSSDSEDEDKK\KENR RKKKKNRSHKSSESSMSETESDSKD SLKKKKKSKDGTEKEKDIKGLSKK RKMYSEDKPLSSESLSESEYIEEVQA KKKKSSEEREKATEK
4875	10372	A	5181	18	566	AEQSGEAARGPVAGPLRPSLWPGFP RRATVCSVQHHGEAGQSGWPYMN PNSNGEIKGSQSQSSGPTIQDYLNRP RPTWEEVKEQLEKKKKGSKALAEF EEKNE*ELEERTGKTQGEIVKWK*E LIQKKDRERKKKRRNLVGSSSDSED EDKKQGKRRKKKKNRSHKSSESSM SETESDSKDSL
4876	10373	A	5182	27	382	SVILSFFFFFFYIAWATVRLCLKQTN ENNDKRDLTSLKVVRK*TLNLHPSI KAMIIRLYFEQLYDNRLANLDEMDI FLATQKLPKLAQEEVKNFSRCVTM DYVNNQNL*TNKGPEPDD
4877	10374	A	5183	2	342	GRSCDPKSVGQTLCVALLSVPLPGD PGQRKLPSQNSEEEL*SQKCGPNPM CCSFPVPLAGGPGHSRRSTQSRTR*L KPQLPGWRTEKGAPEEIGKMMLQV IDERPGSALSCRC
4878	10375	A	5184	2	147	AETGFHHASQDGLDLLTS*STRLGL PKCWDYRREPQRPADTWFLKSTT
4879	10376	A	5185	8780	9035	LALQVHTMTPSKFFFIFLVETGFHH VSQDGLDLLTF*STRLGLPKCWDYR SEPPRPAYFYIFLRRSLSLSPRAGVA VSRDHATAL
4880	10377	A	5186	75	355	SNKNPSISCPRTWGECVCQATSRST WFLYPMPSYAPIKPTPGDVPGTAPS GRPDSTPS**HRLQGTLPKPAPPLLG VFPKPLLAPLFPEGPGP
4881	10378	A	5187	262	354	VWSPPPLTWCLVCQCRYY*PGLLM

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						MCFILPT
4882	10379	A	5188	1	104	ESETLPGGVAHACNPITLGG*GGRIT RSGV*DQP
4883	10380	A	5189	1	144	RDKVFALSHRLECSGAIIAHYNLQL LG*NNHRVSDSPVAGMAGVCHHT
4884	10381	A	5190	99	241	CFPGAWVRLQLTQASDGPWQCSSS QRLHHAPHVVTLYLCCAFSPCSPVK LRDFESAVNNFEKALERAKLVHNN EAQQAIISALDDANKGIIRELRKTNY VENLKEKSEGEASLYEDRIITREKD MRRVRDEPEKVVKQWDHSEDEKE TDEDDEAFGEALQSPASGKQSVEA GKARSDLGAVAKGLSGELGTRSGE TGRKLLEAGRRESREIYRRPSGELE QRLSGEFSRQEPEELKKLSEVGRRE PEELGKTQFGEIGETKKTGNEMEKE YE*SHR*R*GSSVLVLDGDIAQEHG GKDGAEQLSDASLGPGSDYSSHKL LMGPGSARVARGSIMHHTLSHSTC VVPSPLALQ
4885	10382	A	5191	303	427	IVLFEKKIFFFFFETGSCSVPKAGVQ WCGHSSLQP*PTGLM
4886	10383	A	5192	82	352	RVPERVLPRPIPPASCPVSPPASRPL* GTPRAAPETRRRPRTARDPRGLRW QTQPAAPLLASPGPGVAPVASGAPI SRNDFQLCKARMLL
4887	10384	A	5193	1	248	QKLKKLARHGGACACGHKLLGWL RW*DHMSLRGQGCSES*SCRCTPA WTTE*DPVYQHKILSL*DFLI*KASS NRSSVIYEL
4888	10385	A	5194	3	370	AQWRVDSDGAPKRIADSATSPKLL YVDRVVQEILETERTYVQDLKSIV* DYLDCIRDQTKLPLGTEERSALFGNI QDIYHFNSELLQDLENCENDPVAIA ECFVSKSEEFHIYTQYCTNYPR
4889	10386	A	5195	28	183	YDRKRPVGKEKIGKLDCMKT*NFC ASKNTIKEMKRQRTVWEKIFAHYIS ERK
4890	10387	A	5196	1	681	MHPIGIALSKVPVESKEGDIMSHTG GSVPYLDNLNKASVCRGQSCRVFQ VKEMVTQVESENNQEEQKQVRLPE SRLTPWEVWFIGKEKEERDRLQLK ALEFKEDWKLLKRRVTKKSGSVSV SISSQG\NLTVCDCCESFLLTKPVSC KHLIKSHSCPALAVAS/CQRPEGYW SDCGTRSHSDYADEEDSFVSDSSDQ VSSRRTVTHSYAPPQSQPHHRHTQT GTTATYL
4891	10388	A	5197	1	2862	MPGPLGLLCFLALGLLGSAGPSGAA PPLCAAPCSCDGDRRVDCSGKGLT AVPEGLSAFTQALDISMNNITQLPE DAFKNFPPFLEELQLAGNDLSFIHPK ALSGLKELKVLTLQNNQLKTVPSEA IRGLSALQSLRLDANHITSVPEDSFE GLVQLRHLWLDDNSLTEVPVHPLS NLPTLQALTLALNKISSIPDFAFTNL SSLVVLHLHNNKIRSLSQHCFDGLD

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						NLETLDLNYNNLGEFPQAIKALPSL KELGFHSNSISVIPDGAFDGNPLLRT IHLYDNPLSFVGNSAFHNLSDLHSL VIRGASMVQQFPNLTGTVHLESLTL TGTKISSIPNNLCQEQKMLRTLDLS YNNIRDLPSFNGCHALEEISLQRNQI YQIKEGTFQGLISLRILDVSRNLIHEI HSRAFATLGPITNLDVSFNELTSFPT EGLNGLNQLKLVGNFKLKEALAAK DFVNLRSLSVPYAYQCCAFWGCDS YANLNTENNSLQDHSVAQEKGTAD AANVTSTLENEEHSQIIIHCTPSTGA FKPCEYLLGSWMIRLTVWFIFLVAL FFNLLVILTTFASCTSLPSSKLFIGLIS VSNLFMGIYTGILTFLDAVSWGRFA EFGIWWETGSGCKVAGFLAVFSSES AIFLLMLATVERSLSAKDIMKNGKS NHLKQFRVAALLAFLGATVAGCFP LFHRGEYSASPLCLPFPTGETPSLGF TVTLV\LLNSLAFLLMAVIYTKLYC NLEKEDLSENSQSSMIKHVAWLIFT NCIFFCPVAFFSFAPLITAISISPEIMK SVTLIFFPLPACLNPVLYVFFNPKFK EDWKLLKRRVTKKSGSVSVSISSQG GCLEQDFYYDCGMYSHLQGNLTVC DCCES\FLLTKPVSCKHLIKSHSCPA LAVASCQRPEGYWSDCGTQSAHSD YADEE\DSFVSDSSDQ\VQACGR\AC FYQ\SRGFP\LVRYAYNLPRVKD
4892	10389	A	5198	2	413	VDFFFFLRRSLATVAQAGVQWRDL GSLQAPPPGFTPFSCLSLPSSWDYRR PPPRPANFFVFFFF**RWGFTVLAR MISIS*PRDPPTSASQSAGITGVSDRT RLDFKKKKKYCGKKDIMYRKVYTS LIQLTKKSLIH
4893	10390	A	5199	1	142	RKMFGNGRARSGVIVLPCGKGYQS **GGQAVGSGSASCLPLSLCTFP
4894	10391	A	5200	1	375	GEATMNPSHEAEVVCDVPTWWPP VSTR*MGGRE*RKERAEKGRGKGG MEKEGAGERRGKEKNGDSRERGRE GKSVTDNST*GAAAGLPQSPCPIQA RGVQSPRPQAMSRGEPEYSGIGGW GSGEA
4895	10392	A	5201	109	331	PLYCSPGASYMTLTALGPTQTQVPE QRLFVTCILCQEEQEVKVESRAMVL AAFVQRSSVLSKNRCKFI*DPGKS
4896	10393	A	5203	2	168	FFLDSTLKA*AIKAKINKWNDVKLK SFFKTKETINKM*QPMVWENIFANH LSDKG
4897	10394	A	5204	107	357	DLRWYSSFLWMCCIPGAKWHPING SSCVMMGMIKYDFTGHWIVKHIGL AADLDSFYEYLLKSYILFGE*DDL* MFNAAYQSIQ
4898	10395	A	5205	3	376	CQSQVPTDHGGQPPGSHPGWKPGP DLPPRFPDPEPSRPGN*GLLGPALCP SDLYAFGPQGISVNQGLPQWRPGW GHPWRLPEPDS*APAIPQPLAEPVL WGWGGQRPRVPQQLPTAERCCSDF

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						S
4899	10396	A	5206	1	262	QNIFLHLFFCSFTAQKYPMVHLLQK SDNSFNQELLKSMVKSIKMNDVYG PMSQILETLNKCPHFKRQR*VLLLD EYIVLLGRFILFA
4900	10397	A	5207	2	296	NGTHASYGAFYLEYSLLAEFTLVV KHKLPGVYVQPSYRSALMWVGVL SMWEGG*RQGLVRSTVGLGGAVLS SEDRSWGVGSLLSRASAPRLPLAHL RC
4901	10398	A	5208	30	280	FYYAFKEEIIPVLYSLFQKIETGGILL NSALLLIPKST*YRRPYKKGKLNYR PKSFVNINVKILNRILANQIQKCIKRI TYYS
4902	10399	A	5209	1	277	NFSSLLIHGRMHTGEKPYECKNCGK AFTSAKSLQNHGRTHTG*KPCECKQ CGKAFICSSSCQRHEETHSVNMHSV ILIPLKHRKRVGKGPLR
4903	10400	A	5210	220	585	EILVRSLRQDPLRSRRGKRHTGRRW DGSGWRATGARE*RRESRGWEME AREAGRRKPASERRKGSGRRAGDF LEPATRSRSEKEVRTLARNGRP*AS PGSHRSSQ*LQPRVACGGRAATKSS
4904	10401	A	5211	1	291	SFLETLLPRLGCSDAIMAHCSLELLG YMRSCHLSLPS*DYRPTPSRLANSFF LIHGGFFTLSWADLQLLGLKQSFRK SWGLTGVSHHAQPFFPYYLY
4905	10402	A	5212	228	379	
4906	10403	A	5213	317	534	ATKEN*INWDLIK*NKQKPFASKDT TKQAKRQHIEWEKKVVNPIYDKAP VSRIKNLLKLNNKNTNNLIVKKK
4907	10404	A	5214	3	366	IGY/NPDTVACV/PILGWNGDNMLE QSANMPWFKGWKVTRKDGNASGT TLLEALDCILPPTRPTDKPLRLPLQD VYKIGGIGTVPVGRVETGVLKPGM VVTFAPVNVTTEVKSVEMHHEAQK AK
4908	10405	A	5215	1	1254	
4909	10406	A	5216	33	1472	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLKAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GFVEFE\AGI\SKNGQTREHALLAYT LGVKQLIVGVNKMDSTEPPYS\QKR YEEIVKEGSTYIKKIGYY\PDTLAFEP ISGWNGDDMLEPSANMPWFKGWK VTRKDGNASG\TTLLEALDCILPPTR PTDKALRLPLQDVYKIGGIGTVP\VG \RVETGVLKPG\MGVTF\AP\VNVYN GK*KSVEMHHE/AL*SEALSWGTNV GLQLSRNVSVKDV\RRGNFAGDSK\ NDPPMEA\AGFT\AQVIILNHP\SQKN ARHMPLELDCHTAHIACKFAELKE KIDRRSGKKLEDGPKFLKSGDAAIV DIVSG\KPMCVESFSDYPPLGRFAVR DMRQTVAVGVIKAVDKKAAGAGK

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						VTKSAQKAQKAK
4910	10407	A	5217	178	566	KGGATCPESPQDRKRRGNLDMEKL YSENEGMASNHGKMENE*QPQDQR KPQVTLYSGRQEVRKRGKDRKQGQ NRR*GNV*RIKGKPESEGEAKEGKS EREGESEMEGGSEREGKPEIEGKPE SEGEPLE
4911	10408	A	5218	27	336	TNPVQQTLVPIWTSTRLPDTHEDKA FSAPQIEDRGTPGLGSRGPALGPSPT PDCAG*VVAAGPGPAESHPRAPKPT AGMSPGVARLSSPGSGSQGSWQNQ ERP
4912	10409	A	5219	2	454	HFNMRDPLTDCPYNKVYKNLKEFS QNGENFCKQVTSVLQQRANLEISY AKGLQKLASKLSKALQNTRKSCVS SAWAWASEGMKSTADLHQKLGKA IELEAIKPTYQVLNVQEKKRKSLDN EVEKTANLVISNWNQQIKAKKKLM VSTQET*STADLHQKLGKAIELEAIK PTYQVLNVQEKKRKSLDNEVEKTA NLVISNWNQQIKAKKKLMVSTQET
4913	10410	A	5220	26	130	TTWKYQYKNLERNQKEITELKSTIA EIENITRGI*R*FEQTKE*INELEDKI MEIFKDKR*KKGEKSLRGLWPPSRD KEACMPWKLQTEEKKKGAERLSEE IMAESFSNLLADMNINS*ELKSTIAEI ENITRGI
4914	10411	A	5221	48	394	SPSMCGSLDPPTLPQTWLQVPSMLT HPCPPPPPHCPPLAHPPSSLLPSTHIY H**HLSPPYPNPGTQEGHSGVRLRA TDVASPSVLGQFPSYSISVPREGHA ATVAAKGPLECRA
4915	10412	A	5222 .	3	726	EQEVDYDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCCKHPEA KRMPCAEDYLS\VVLNQLCVLH/EK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCCKHPEA KRMPCAEDYLSRGPEPVMCVA
4916	10413	A	5223	4274	5256	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT

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						KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNIILPKFNHLCTHTHTHTHLTLFST YLKNDRDKTIMCKLSLIG*L\ESLEF GGSGENVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWLDLGT LSV
4917	10414	A	5224	1	332	RMPCAEDYLSVVLTQLCVLHDKTP VSDIVAKCCSESLVNSQACLSDL*V KDAYVPKEFNTETFTFHADICALSE TERRIMKQTGLDEFVKHKP*ASDER LSAVMDDFAAF
4918	10415	A	5225	7	564	TTRAAGREALSPGQGAGGGEGGAE PRHTATGHAAGREGRGGRGADQG* GWPRGARALHDQAEGRGGLPAGLP VQAERPQREPCSGQVGSEPPCHP\A TAGGRKVRPAWPAAAGEAGGHSG TGRAGAAGGAAVGTGGGAAGPGG LPMSGGAGPGGSGAAAPHAAS*VQ PAAGAASAATRNRIMPKTT
4919	10416	A	5226	132	917	PGLFYLGEEQPGPQPAGGPAAGQG ATAGAEEAAGCPGGAAAPAVLAG GRAGGRSAGWCAGAPGA*PGLFYL GEEQPGPQPAGGPAAGQGATAGAE EAAGCPGGAAAPAVLAGGRAGGRS AGWCAGAPGA*AQP*TTGAAGREA LSPGQGAGGGEGGAEPRHTATGHA AGREGRGGRGADQG*SLSQATDLW TSGPSHKWTDLSLWPYPCCSGCSW GQCL*LRAEGRGGLPAGLPVQAERP QREPCSGQVGSEPPCHPVSHTPKGP VPHCLGASPGLLWLATAGGRKVRP AGPAAAGEAGGHSGTGRAGAAGG AAVGTGGCQQRWIR
4920	10417	A	5227	3	1245	AWEFVWHPGGFDRSCPGPQGGEGS EGGEGT*EGSGSLALRPRPLSCPRA GPGPGPRLA*ASVYPWNQKRVGGL WRPQRTPARLCDPHAPEHAWAL*G KPGPAGHPAEAA*RQRE*AAGPRGT AAAPAGQDRQHHAGPRGRPARGA AAAERQRAPEKGEEQPGPQPAGGP AAGQGAAAGAEEAAGCPGGAAAP AVLAGGRAGGRSAGWCAGAPGA* AQP*TTGAAGREALSPGQGAGGGE GGAEPRHTATGHAAGREGRGGRG ADQG*SLSQTTDLWTSGPSHKWTD LSLWPYPCCSGCSWGQCL*LRAEG RGGLPAGLPVQAERPQREPCSGQV GSEPPCHPVSHTPKGPVPHCLGASP GLLWLATAGGRKVRPAGPAAAGE AGGHSGTGRAGAAGGAAVGTGGG AAGPGGLPM
4921	10418	A	5228	612	795	PGFISAIGGLVGLSSYDFYEYKEYED KPTSPPIAEMNPGYNI*HDLIKSFKM LAFICSISS
4922	10419	A	5229	1	345	SSWSFTLVTQAGVQWHDLGSLQPL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PSEFKRFSCLSLPSSWDCRRLPPRPA NFLYF**RWGFTILTSLVLSY*PCVS PTSASQSAGITGVSDHARLIVGDFN TPLLITERSSTQKI
4923	10420	A	5230	1	1212	MPKKRQALVEFEDVLGACNAVNY AADNQIYIAGHPAFVNYSTSQKISRP GDSDDSRSVNSVLLFTILNPIYSITTP TRLNVFKNDQDTWDYTNPNLSGQG DPGSNPNKRQRQPPLLGDHPAEYG GPHGGYHSHYHDEGYGPPPPHYEG RRMGPPVGEYGPHADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVEKV KISLKKQSPGGRPMGEEWL\DGYAV DRAITHLNNNFMFGQKLNV/CVGA QAREGSRGTGERKGGEWGPAEEHS EAEVLTHTEMGCGSVSKQPAIMPG QSYGLEDGSCSYKDFSESRNNRFST PEQAAKNRIQHPSNVLHFFNAPLEV TEENFFEICDELGVKRPSSVKVFSGK SERSSSGLLEWESKSDALETLGFLN HYQMKNPSINLVT
4924	10421	A	5231	1	421	FDPPGCFFTPIGNPFGPFQGNFHFRK NGVQAMVEFDSVQSRQAAKASLN GADIYSGCCTLKIEYAKPTRLNVFK NDQDTWDYTNPNLSGQGDPGSNPN KRQRGTVISQD*PSLLKNYCTCDFF FSCSYICAAHVLCGTFQ
4925	10422	A	5232	2	1883	DEQRRRSGAMVKMAAAGGGGGG GRYYGGGSEGGRAPKRLKTDNAG DQHGGGGGGGGGGAGAAGGGGGG ENYDDPHKTPASPVVHIRGLIDGVV EADLVEALQEFGPISYVVVMPKKR QALVEFEDVLGACNAVNYAADNQI YIAGHPA\FVNYSTSQKISRIDE*ND YR\SVNSVLLFTIVNTINWITTDVLY TMCNPCGPVQRIVIFRKNGVQAMV VFDSVQSAQRAKASLNGGDIYSGC CTLKIGYAKPTRLNVFKNDQDTWD YTNP\NLSGQGDPGSN\PNKRQRQPP LLGDHPAEYGGPHGGYHSHYHDEG YGPPPPHYEGRRMGPPVGGHRQCP SRYGPQYGHPPPPPPPPEYGPHADSP VLMVYGLDQSKMNGDRVFNVFCL YG\NVE\KVKFMKSKPGAAMVEMA DGYAVDRAITHLNNNFMFGQKLNV CVSKQPAIMPGQSYGLEDGSCSYK DFSESRNNRFSTPEQAAKNRIQHPS NVLHFFNAPLEVTEENFFEICDELG VKRPSSVKVFSGKSERSSSGLLEWE SKSDALETLGFLNHYQMKNP\NGPY PYTLKLCFSPAQHAFLIRCLGRVPFE QENISLSFMPFFGFCFCYLQKILGSP FFFFFFFFLKARVEEGFPPP
4926	10423	A	5233	2	337	DMILAERGGVCVMMKTQCCTFIPN TSTTDGSITRALQGLTALSNELANN SGVNDPFTGWLEK*FSKWKGIIASIL TSLAAVMGVLILVRCCVIPCLQRLM QRLIKMALTQTS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4927	10424	A	5234	62	343	RQLNRNDPNRNKGKKVGIKQCLRF WNNFILTCLIGVSEIEEKKNGAE*IF EEIMSKNFPKLIKYINPQIQEA**TPS KINTEKTTFRH*IIKGR
4928	10425	A	5235	1	359	TDDDLNWLDHSRTFREQGVDETET CLLRRKFSYSDQNVDSRDPVQLNLL YVQARDDILNGSHPVSFEKACEFGG FQAQIQFGPHVEHKHKPGFLE*MTF CFSFFSFLLSSFSFSFLFLS
4929	10426	A	5236	2	264	SYYPRGEISVPFFNICHFFLSCFYNLS RFFCKKSPASPLCFSIKKSPFVKIHL VFSLVTSSFLK*FFFYL*FFPESVISF GSFSNSD
4930	10427	A	5237	3	246	LIPRGQGSTVVLPYNPATSIFGNDLN EIKMYGHAKTCIWMFMTSSFIIDRT RKRQ*CSSVREWINKQ*CIQTMELV FGRN
4931	10428	A	5238	78	411	VLNSPICNCLYPILCSFLFLIIYFVVC FYTFIPVFYLVYHQEIVI*SLTLVFFV CVVKINTRLMVHIFILYICL*LSICNS VYLLHVHIYLEHFL*HILMVVFFKR SDQSS
4932	10429	A	5239	2	175	TKLDFIGIKGFSSVKDNVKGMRRQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4933	10430	A	5240	1	335	VTIRGAGIPDESRNVNYSLASFLKR WLTLMDRGFIFNLINDYISGFSPKDP KVLAEYKFEFLQTICNHEHYIPLNLP MAFAKPKLQRV*DSDLEYSLSDEY CKHHFLGGLL
4934	10431	A	5241	139	354	SPCLPYCCLLCYRYGDGRIMIGFSC GH*VVISTHTGELGQEIFQARNHKD NLTSIAVSQTHIKVATCENNLP
4935	10432	A	5242	2	332	ILAGAII*DNEIKLM*IEKEVVKLFLF TDDMILCVENSKEHTHSHTQLLGLI NEFSRASG*KINVQKLFLYTNNVQS KNEIKEPSLCTKASKRIGYLGIHLTK EV*DLYSERTKPH*KKNRILRNTFN KRSVRLVQ
4936	10433	A	5243	137	290	GSSDINQTKHVRS*VNRQICSRTTQ QSPEDCDFKKDGLVKRCMGTQTRQ SL
4937	10434	A	5244	1	363	LTCSGDKEQIKDKSHVLKGKGNFE RETS*KKK*SLPPFDDNVEPNDLYV EENICSKSDSERPRSASSSSRSSSSFT PSQTRQQGPLKSMMNDLHSDDYEE ESDEMEDNGPDFEMGKPVNIR
4938	10435	A	5245	2	376	VHLGWCMLPLRTHTEYVKALSYA* DKQLGA*AGLDRQIFLWDANTLSA LTASNNTVTTSSLSGNTDSIYRLAM NQLVTIIVSGSNDKALRVWDPLTCA TLVNLKGHTDNGKALVFNRDGTQC LSR
4939	10436	A	5246	60	185	
4940	10437	A	5247	1	146	RWRDLGSPQPAGFR*FCCLSLLSSW DYRHAPLF*QFYLFILLFCKKYF
4941	10438	A	5248	2	298	TFFTPFPVAKPNPRGPKTPAPYFSPQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GPQKIYPPKFLGPPFNFPPPLLGKVF RAPNPRV*LPPGARPSSSSSLLPGF* KIPKPLFY*KKIFPTPQKTKK
4942	10439	A	5249	77	370	EYS*SVVFLDLMRRQEELRRMEELH NQE
4943	10440	A	5250	83	467	YSEKSAGLWLNMLEKSLPGHRDTA TQIQHVSPMCQVEPPAKKAATLAE GDKDNDI*PCFVQRQLREGRQGRA ARLWEKWLRWYVEKKAKKTALV VKSSIPLDIKPWDNETNIAQLEACM RFIQLDGLV
4944	10441	A	5251	1	359	KYTLSRLATVPPTLNPAEYNISPDTR RAQVEQLAIRAGLK*EYLLQYNNP NRRGLIEDPALIRWTYARSANVYPN FRPTPKNSLLGALCAFGPLFFWYCV FKTDMDRNQKLIREGKLDQ
4945	10442	A	5252	3	349	SSLATVPANLNPAEYSISPDNRRAQ VEQLAIRAGLK**YLLQYNNPTRIGI IKDPALIRWTYARSANVYPNFRPIPK NSLLGDLCAYGPLFFWYCVFKPDM DRKETLIPEGKLDQ
4946	10443	A	5254	1	415	NAVIQVAHPLVQKQ*VDYIHNGFL VPVMGPALHKTSVEEMIASTAYLEL FLRSISEPALLRTLLRFLLLHRHDTH TILDTLVARIGSNSRLCMVSLSLFKT LLNLSCEDVLLQLGLRYLVPCNHV MLSQKPAVRDVDL
4947	10444	A	5255	34	394	YRHYTICCIIGFLNTITMMTVSFHKY GEYFPGT*DLRDIDAGKC*YYAVNF PMRDGIDDESYGHIFKPIISKVMEM YQPIAVVLQCDAYSLYGDSLDCFNL TIIRHSTRLYLI*SYHFTS
4948	10445	A	5256	178	417	ILVPPAGGKGPNLI*WNPGPPGARG FPGLTPPRGGKKGRAQPPPENLVF* EKTGFPIVQRGGLKPPPGPPKGGE*R GGPP
4949	10446	A	5257	749	1049	DGSSLLGPRPGGKGPNQTKGNPRPP G*RESPPHPPPRRGKKRMAQPPQLI WDFSSSSGFPL*QGGGINPHPDPPKG GKKRGEPPEPTTGPSKRGKKQGFG
4950	10447	A	5258	1	359	LFPKVNLSPVTPAKDTGLTAAPQEP KAPKASPVQHALPSSLSVPHTAILV TGAQLCGPAVNLSQIKDTACKSLLG LEEKKHAEAPAAENPHGGPGDSSA PY**GDAPKGHAIRAVEVPD
4951	10448	A	5259	1	441	FFFLNRVLTLITQAGVQWCDHGSLQ PRSLGLK*PSHFSLPSS*DYRCAPPH LANFYIFYKDRWGFTMLPRLVWEL LGSSDLSILDSQSAGITGVRHHTWA NFFNFLCVSGIN*RNFYNKFTSWGS HPNSQYYSGISWGQSTNILLGY
4952	10449	A	5260	1	553	FYFYFFFFPLFFFFKPQDDFLVPGDQ NQRPGGSMPLGTAFILFQMKTLSLV RRGINQDN*HWRQEDPLIPISPGFPS RIPPLKSEMSLPLSTDGSETRRTQSP FDEIYMAHDASGLRLPDSPPPPAAP GRDPAPSGQRAPGKLRGQCQLKSE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RESRKEERQRSKPGEAAALGGVAC TFHLKSRS
4953	10450	A	5261	1486	1695	GKSCRPVNIYFILFSSFLRRSFALVA QAGVQWCDLGSLQPPPPGFK*FSCL SLPSSWDYRYPPLCPANFC
4954	10451	A	5262	1	334	RRFVSQETGNLYIAKVE*SDVGNYT CVVTNTVTNHKVLGPPTPLILRNDG VMGEYEPKIEVQFPETVPTAKGATV KLECFALGNPVPTIIWRRADGKPIA RKARRHEGCEM
4955	10452	A	5263	78	313	KVTYIQKNVYSKCTAGWVFTQRAR VGSREPFPAAPSPGPHGGDPPSPPQL G*PLSPLPQPAPVRLPSPVMMSERIL PF
4956	10453	A	5264	3	320	IFSQENL*YSDGSDILGLLALQAEEN LGMVMIFTLVTAVQEKLNEIVDQIK TSSSSSSSSSSSSSAEEAEKQLFHGTP VTIENVLNWESQGWRRQTFLGKILE KEKG
4957	10454	A	5265	3	941	APPRCLGDLWARARATMTDYGEE QRNELEALESIYPDSFT\VDCTLIQPS *QLVFQNINGLS*YHILLQ*CFT*QG PC*VLSENPP\SFTITVTSEAG\ENDES IHIKLLSCVLAVQTTLKFTYSEKYPD EAPLYEIFLPGKILEDN\DVSDILKLL \ALQAEENLGMVMIFTLVTAVHERI NV\LVDHIITRCEVEMKL*DKEAEE AVKQLFHGTPVTIENFLNWKA/RSF DAELLEIKKKRMKEEEHAGLDKK\S GKQLFETDHNLDTSDIQFLEDAGNN V\EVDESLFQEMDDLELEDDEDDPD YNPADPESDSAD
4958	10455	A	5266	1	332	LKKHKSTRVP*NVKSGK*NFSPPFKI RPWAQKRAKKKGAREKKAD*EKG EFGKLSSSSRFRPGKKV*G*PKGFQR NFEKKPVKSQGPVNMGVIPAFEKKP RIPPVAKIPI
4959	10456	A	5267	3	375	SASPQTLQQSLPRSIAPKPLTVRLPM NQIVTSVTIAANMPSNIGAPLISSMG TTMDGSAPSTQVSPSVQTQQHQMQ LSSSSSSSSSSQMQQMQQQQLQQHQ MHQQIQQQMQQQHFQHHMQ*HLQ Q
4960	10457	A	5268	1	360	KGAPKHGQAPLGDPPRAVGGQEH* GPARGRGPGPREPGSGQTSSPWVH VRPGGGKNDSGKARP*ILDPKSVSC IPAPSSHRPLSSPTPNPFP*SSYEGSP RSPQPWTLQPQGPWPPSRQA
4961	10458	A	5269	1	181	KKKPQTWEKLV*GLF*KKRNPGWG QRVPPVTPPLWGVKKRGGVFFRGL KPPLKPRENPFF
4962	10459	A	5270	10	108	SHINVPMNQP*VVSLGPGQVTKGW DQGLLVMCE
4963	10460	A	5271	1	336	EFLGAVGFCRLWIPNFAVLAKPLYG VTK*GDTELFKWGSQQQ*AFHELK EKLMSAPALGLPDLTKPFTLYVSER EKMAIGVLIQMVGPWPRPVAYLSK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ELDGVSKARSEGCE
4964	10461	A	5272	1	118	TEVRHGKLDSSKWIPIRGN*NIYNP HCLSYKLEHGSDQEIPSDWYPFATV QFSVPDLC
4965	10462	A	5274	2	327	SCLVLVLLCVEYLFPYLHFQSICVFT GEVSFLQAAYSWVMGFFVFLFILIH SYFL*LLWGLFISLHLWLSLTCEDLF LLFFSRCLIYIICFVFLLFMSFLILWR LLVF
4966	10463	A	5275	171	331	LKTSFRTKTCT*MLTASLFVIAKTW KQPRCPSVGE*LSNL*YVQTMECYS VLK
4967	10464	B	5276	83	332	MGKRDNRVAYMNPIAMARSRGPIQ SSGPTIQDYLNRPRPTWEEVKEQLE KKKKGSKALAEFEEKMNENWKKE LEKHREKLLSGX*
4968	10465	A	5277	76	138	
4969	10466	A	5278	1	1050	
4970	10467	C	5279	146	433	MKKKSNERWDQVYKILKGKSLRPG FPRCATVRAIQHHGEAGQSGGLYEP NSNGEIKGSNPVFRANNTGLSESTK AYLGRSKRATRKEKERLQGFG*
4971	10468	A	5280	27	264	NPNHQSLLCRAFCGVLILILPVLALL TRLSFGELTLYNNHFIYIFKAFFKFI* VFKWTGDNMFFIKGDMDSLAFGGG G
4972	10469	A	5281	135	358	VHSPVL*LISTIPTSRLKFLKETGHGT PMEEIPEEELSEDVEQIDHADRELRR GQNLRCKGIHRLPTHIQVGQN
4973	10470	A	5282	15	196	KGKIVKLDFIKI*NFFSAKDPVNY*K DNYRLRKMTANHISDKEFVSKTYK ECLKLNLKKF
4974	10471	A	5283	307	383	YF*VSLATLCVYFLLDEGNILTATK VFTSMSLFNILRIPLFELPTVISAVVQ TKISLGR
4975	10472	A	5284	3	267	TIVRPYLLKKKTGTIVEERVNAPGW NEDDDVSVSDESELPTSTTLKAFEK STMEQLVEKACFRDYHRLGL*TLSG SCCRS*P*SRRVQ
4976	10473	A	5285	1	260	TAVPSAASMTSTRAASASSVHVPVS ALGAGSAATAASEEMQTIPQATAA KYPRTIHPESSTSASRSLGT/TISSHP VSHKCSFHKSG
4977	10474	A	5286	60	292	VTNFLIFHMRIISKYISIFLTVFFFVSQ IVLLFKHSYFSYLELWKMQK\RDSK NAT*KRAL*RFHEKSFHEGCMCIKS
4978	10475	A	5287	738	1152	KGRVWSWCSRKRTFCSFGSFSSSDA LTSYITTAAIPT\TAVGGASATAVPS AASMTSTRAASASSVHVPVSALGA GSAATAASEEMSDKELITCTRQLKR DGCFGQYTNQPGTGNMGKKQPRIT LCPLNKRKVVAVKPN
4979	10476	A	5288	3	555	RKRTFCSFGSFSSSDALTSYITHCCQ SPPAAV*LASATAVPSAASMTSTRA ASASSVHVPVSALGAGSAATAASEE MYVPRVVTSAQQKAGRTITARITGR CDFASKNRISSSLAIMGVSPPHELSC

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						CGKTSSQSTVQTHSLKQLPAKYPRT HSIPESSTLSLPRSLGTQISSHPVSHK CSFP
4980	10477	A	5289	94	323	VIGYRNIRCTILTSTITSSLSIL*LNH* PETRLSE*AGV*DKGLVVAQMMWL MDHIFKYTNFGIVSLVHGDFFIRQ
4981	10478	A	5290	2	319	MVLVTLDDKYAVAALWGKVKVDE VDGEALGRLMVVYPWTQRFWES* GDLSPPDADMGNPKVKVHGNKVL GAVSNGQAHVDNLKGTFATVSEM HCDKLHVAQEPEVL
4982	10479	A	5291	1	159	RDLQHFPSSVAM*DQTQNDIASTSN HESILQGIKGQSQL*EEVQLME*APV DC
4983	10480	A	5292	187	282	LRSY*CLLLMISFTRNANLFRLHGT HTDTFKCLEYEKCFNCNSDLIVHHR INMDHNPHQTSA*DSGLLLGMHF
4984	10481	A	5293	1	156	SGGVDEQMMREKEELMLWLQDYE EKIKKAEREL*EQIKREMKKNQKRK REKK
4985	10482	A	5294	179	322	NKVGGLTLPNCKTYYKATIIKTVW YWRKKRQIGQ*NRIESPEIDPHKY
4986	10483	A	5295	2	395	RDRESDRDGQRRERERRTRKWSRS RSHYRSPSRCRTKSKSSSFGRIDRDS YSPR*KGRWANDGWRCPRGNDRY RKNDPEKQNENARKEKNDIHLDAD DPNSADKHRNDCPNWITEPINCGPD PRTRNPEKL
4987	10484	A	5296	3	228	HELPHPGLGLKRGCWVLEVAEHVV LGKALLILLPYRFKRNILAMDDKTG MTRNPHFSHNNWIPTFFSTQYFWIIF KVRWPRLKDTTDLRILAPNCLADR LSRHRCNIWQFMQGIRPLVLNFGSC T*PSFQPQQLYTNLFQHPVFLDHL
4988	10485	A	5297	61	360	YVSNSKCSNHRK*SLSSSSSSERESS FVPQVELHGRDLG*LQLWLPGFGK FPGLTPLRNGDDGPRPQPPANLGLL VKTGFSPVAHLGVNLGTLGDCPAL P
4989	10486	A	5298	124	351	EREFRFVPQVELHDRDLGSLHPGTP GLRKFSGLTLPRSGDNGPGPPPPVN LGFLEETGFSHVAHFGLNFGT*GDC P
4990	10487	A	5300	3	388	HERHERHEGALSQDALLRISIPLDSN MRPEKCRRFVHPQRQLLHLNGTFP NTSDADMEPCVDGWVHDIISFSSTI VTE*DLVCDSQSLTSVAKCAFMTG* TADGFLGAHLSHRVRASSNVCMGG SIVC
4991	10488	C	5301	47	269	MPPLIQSGMSSRTKTRTSSPCWNVH PAPEQYEAPDKDFMIVALDCSAAW PRAWVVTWSSWCPQQHHDIAVPV HA*
4992	10489	A	5302	1	253	MYTQ/HPEQYEAPDKDFMIVAL/DL LSGLAEGLGGHVEQL/VARSNIMTL LFQCM/QAEFMPILGTNLNPEF/ISVC NNATWAIGEICMQW

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4993	10490	A	5304	229	2984	PCPCQNFLRCSTSFNFSLPCAMDWQ PDEQGLQQVLQLLKDSQSPNTATH RIVRDKLKQLNQFPDFNNYLIFVLT RLKSEDEPTRSLSGLILKNNVKAHY QSFPPPVADFIKQECLNNIGDASSLI RATIGILITTIASKGELQMWPELLPQ LCNLLNSEDYNTCEGAFGALQKICE DSSELLDSDALNRPLNIMIPKFLQFF KHCSPKIRSHAIGCVNQFIMDRAQA LMDNIDTFIEHLFALAVDDDPEVRK NVCRALVMLLEVRIDRLIPHMHSIIQ YMLQRTQDHDENVALEACEFWLTL AEQPICKEVLASHLVQLIPILVNGM KYSEIDIILLKGDVEEDEAVPDSEQD IKPRFHKSRTVTLPHEAERPDGSED AEDDDDDALSDWNLRKCSAAAL DVLANVFREELLPHLLPLLKGLLFH PEWVVKESGILVLGAIAEGCMQGM VPYLPELIPHLIQCLSDKKALVRSIA CWTLSRYAHWVVSQPPDMHLKPL MTELLKRILDGNKKVQEAACIAFAT LEEKACTELVPYLSYILDTLVFAFG KYQHKNLLILYDAIGTLADSVGHHL NQPEYIQKLMPPLIQKWNELKDED KDLFPLLECLSSVATALQSGFLPYC EPVYQCCVTLVQK\TLAQAMMYTQ HPEQYEAPDKDFMIVALDLFSGLAE GLGGHVEQLVARSNIMTLLFQCMQ DSMPEVRQSSFAFLGDFTKACSSHV KPCIAEFMPILGTNLNPEFISVCNNA TWAIGEICMQMGAEMQPYVQMVL NNLVEIINRPNTPKTLLENTGRLTSP SAIPAITIGRLGYVCPQEVAPMLQQF IRPWCTSLRNIQDNEEKDSAFRGIC MMIGVNPGGVVQDFILFCDAVASW VSPKDDLRDMFYKILHGFKDQVGE DNWQQFSEQFPPLLKERLAAFYGV
4994	10491	A	5305	47	411	
4995	10492	A	5306	20	1020	LSLTSRMEEAELVKGRLQAITDKRK IQEEISQKR\RKLGEDKPKA\QPLKT KAL\REKW\LPRWNPASGKEQEEM KKQNQQDPAPRSQVPRTKYPSGLR KRSQDLEKAELQISTKEEAILKKLKS IERTTEDIIRSVKVEREERAEESIEDI YANIPDLPKSYIPSRLRKEINEEKED DEQNRKALYAMEIKVEKDLKTGES TVLSSIPLPSDYFNVTGIKVYDEGQK SVYAVSSNHSAAYNGTDGLAPVEV EELLRQALERNSKSPTEYHEPVYAN PFYRPTTPQRETVTPGPNFQERITIK TNGLGIGVNESIHNMGNGLSEERGN NFNHISPI
4996	10493	A	5307	1	95	GTRTFLRTYLSEIARRHPEFYAPELL *FAKR
4997	10494	A	5308	1	338	GTSLSA*GLNIDGQLGLGHTEDIPY YTPCRSLFG*PIQQVACGWHVTIML TEHGQALLCGCNSIVQLAGPHGHL RRVGT*TIELRRENAVHIGAALMPH

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VALTTSRSIFQCR
4998	10495	A	5309	3	472	VTEFAKTCVADESAENCDKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPNLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGERAF KA\VARLSQRFP
4999	10496	A	5310	12835	13995	TIPIESDIFPSIFYLYLSSLAYADTYE ALSRFY*KKKLINLLLSLN*ATHFPK IMPVVQVELKAKFN*LFR\KCFLPST NPLLCRWR*YDEWNIATS*LIPAKC SLFYLLC*TVSCLAENT*LLFFRLLV RYTKKVPQVSTPTLVEVSRNLGKVS SKCCKHPEAKRMPCAEDYVSL*KHI IN***KNFPFRYC*CYLS*AEGSNVC VCMFCACVCACTCVYV*YWQSRPR G**FFFFF*DGVSLCCPGWSAVVPSR LTATSASQVQAILLPQPPK*LGLQV HATMPG*FFVFLVENFQLHLF*ISAL LPVL*LSVVLNQLCVLHEKTPVSDR VTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQT
5000	10497	A	5311	1	349	GTSKKLANKVVYNVGLCICLFDITK LEDAYVFPGDGASHTKVHFRCVEC HPFLHEILTGKIKGCSPEGAHHPLR* HPDFPLFSRPPAFLSPSQYILSPREIL VHPSILKFRTRRPY
5001	10498	A	5312	1	410	IEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREK MT/QGSVPLPAFPP*SLQIMFETFNTP AMYVAIQAVLSLYASGRTTGIVMD SGDGVTHTVPIYEGYALPHAILRMD LAGRDLTDYLMKIL
5002	10499	A	5313	216	390	GSADARAPPVLSPVIFCPS*FLTGRP LQGVMVGMGQKDSYVGDEAQSKR GILTLKYPIEHGIVTNWDDMEKIWH HTFYNELRVAPEEHPVLLTEAPLNP KANREKMTQVRLGRRPCSSRPFPSH FLPILISDGSSPAGRHGGHGPEGLLR GRRGPEQAWHPDPEVPH
5003	10500	A	5314	4	1254	HAHAKLGTRAASSRTLFFRQLRRR VSLPVAMEEEIAALVIDNGSGMCK AGFAGGDA\PRA\VFPSIVGRPRHQG VMVG\MGQK\DSYVGDEAQSKRGI LTLKYPIEHGIVTN\WDDMEKIWHH TFYN\ELRV\APEE\HPVL\LTEAPLEP QGQTREKMTQ\IMFETFNTP\AMYR GPSRAVLSL*\ASGR\TTGHCHGTLG DGVTHTVPIYGGLPHCSTPFLRLGP GLARDLTDYLMKILT*SEGYSFTTH GPSGKFVRDI\KEKLCYVALDF\EQE MATAASSSSLEKSYELPDGQVITIG NERFRCPEALFQPSFLGMESCGIHET TFNSIMKCDVDIRKDLYANTVLSGG TTMYPGIADRMQKEITALAPSTMKI KIIAPPERKYSVWIGGSILASLSTFQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QMWISKQEYDESGPSIVHRKCF
5004	10501	A	5315	279	418	VEHSISNKENFLGQGTGCHACNLNT LGGRGGRITWRSGV*DQLDQH
5005	10502	C	5316	274	530	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE XQIXKQTALV*
5006	10503	A	5317	2	736	RLAKTYETTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLIKQNCELFE QLGEYKFQNALLVRYTKKVP/SVVL LLRLAKTYETTLEKCCAAAHPHEC YAKVFDEFKPLVEEPQNLIKQNCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLS
5007	10504	B	5318	120	1070	MPADLPSLAADFVESKDVCKNYAE AKDVFLGMFLYEYARRHPDYSVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNFHT ECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEV ENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQN CELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRKPRKSGQQML*
5008	10505	A	5319	2	668	
5009	10506	C	5320	246	365	MDDFAAFXXXCCXXDXKGDLLXR RKVKNLLLQVQLPLGF*
5010	10507	C	5321	261	656	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE RQIKKQTALVELVKHKPKATKEQL KAVXDDFXAFVEKCCKGDXKGELL XRRXVXNLL*
5011	10508	C	5322	158	607	MLCQSVGSKCCKHPEAKRMPCAED YLSVVLNQLCVLHEKTPVSDRVTK CCTESLVNRRPCFSALEVDETYVPK EFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVXDD FXAFVEKCCKGDXKGELLXRRXVX NLL*
5012	10509	C	5323	158	532	MLCQSVPCAEDYLSVVLNQLCVLH EKTPVSDRVTKCCTESLVNRRPCFS ALEVDETYVPKEFNAETFTFHADIC TLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCCKAD XKG*
5013	10510	A	5324	2	740	PADLPSLAADFVESKDVCKNYAEA KDVFLGMFLYEYARRHPDYSVVLL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLIKQNCELF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGK/VCCTESLVNRR

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						PCFSALEVDETYVPKEFNAETFTFH ADICTLSEKERQIKKQTALVELVKH KPKATKEQLKAVMDDFAAFVEKCC KADDKETCFAEEG*KLGAASQAAL GLY
5014	10511	A	5325	1	588	
5015	10512	A	5326	364	1356	TGDHAFQLWKSMKHTFQVSTPTLV EVSRNLGKVGSKCCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCCKADDEMPADLPS LAADFVESKDVCKNYAEAKDVFLG MFLYEYARRHPDYSVVLLLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCELFEQLGEY KFQNALLVRYTKKVPQVSTPTLVE VSRNLGKVGSKCCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRV TKCCTESLVNRRPCFSALEVDETYV PSVNSNSCRGLKKPRKSGQQML*TS *SKKNAL\SEDYLSVVLNQLCVLHE KTPVSDRVTKCCTESLV\KGDHAFQ LWKSMKHTFPKSL/YAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQN CELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVE/VLKKPRKSGQQML* TS*SKKNALCRRLSIPWS*TSYVCC MRKRQ*VTESPISRNLGKVGSKCCK HPEAKRMPCAEDYLSVVLNQLCVL HEKTPVSDRVTKCCTESLVNRRPCF SALEVDETYVPKEFNAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQN CELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCK HPEAKRMPCAEDYLSRGPEPVMCV A
5016	10513	A	5327	1468	1946	LHISWEGEPIDYSVVLLLRLAKTYE TTLEKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCELFEQLGEYKF QNALLVRYTKKVPQVSTPTLVEVS RNLRKVGSKCCKHPEAKRMPCAED YLSVVLNQLCVLHEKRQ*VTESPNA AQNPW*TGDHAFQLWKSMKHTFP KSLMLKHSPSMQIYENQDSISSKLK ECCEKPLLEKSHCIAEVENDEMPAD LPSLAADFVESKDVCKNYAEAKDV

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						FLGMFLYEYARRHPDYSVVLLLRL AKTYETTLEKCCAAADPHECYAKV FDEFKPLVEEPQNLIKQNCELFEQL GEYKFQNALLVRYTKKVPQVSTPT LVEVSRN/LRKSGQLR*I*TSCGRAS EFNQTKL*AF*AAWRVQIPECAISSL HQESTPSVNSNSCRGLKKPRKSGQH TKKVPQVSTPTLVEVSRNLGKVGS KCCKHPEAKRMPCAEDYLSVVLNQ LCVLHE\KTPVSDRVTKCCTESLGG TGRPCFSSSGKSMETYVP\KGFNA\E TFTFPGSFCT/LSWEGEPIDYSVVLL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLIKQNCELF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGKVGSKCCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTKCCTESLVNRRPVC
5017	10514	A	5328	1	2063	MKKVKERDSFIMEDLGAEGLKSSA YSRGVFRRDAHKSEVAHRFKDLGE ENFKALVLIAFAQYLQQCPFEDHVK LVNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRETYGEMAD CCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKK YLYEIARRHPYFYAPELLFFAKRYK AAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERA FKAWAVARLSQRFPKAEFAEVSKL VTDLTKVHTECCHGDLLECADDRA DLAKYICENQDSISSKLKECCEKPLL EKSHCIAEVENDEMPADLPSLAADF VESKDVCKNYAEAKDVFLGMFLYE YARRHPDYSVVLLLRLAKTYETTLE KCCAAADPHECYAKVFDEFKPLVE EPQNLIKQNCELF\EQLGKYKFQNA AISSVTPKKVPQVSTQLLTPTLVEVS K/NTLGKVGSKCCKHPESKKKCPVA E\NYLS\VVLNQLC\LLHEKT\PVSDR VTKIAAQEPL\VNRRP\CFSALEVR* NIPFPKEVNA\ETF\TFHADICTLS\EK ERQI\RKQTALVELVETQAPRQQKE QLKA/VLWDDFAAFVKKIAAKA\DD KETCFAEETISGNGAKKAIFLVNDE FILMSLTLIQNHRTYSSLPPCLYDSK KLLFHYLASIYPFVPPQDACKGVSE L
5018	10515	A	5329	1	339	RRRRKKNEKRKRQRKIKDEKSRKN SLRVEMRETWRQREKQKEEDREKR KGQQEKERRKREIEEKEST*CEQME IGKTKKVNIHCRWQTQLKLKFHLFS LFSIKMSLSSFSTRA
5019	10516	A	5330	2	189	ARGGDAGDAFDGFGFGDDPSD*LS SCHIDVHRYLFSALCDCYTFYFVHI RVFLLSMRLADTA
5020	10517	A	5331	3	346	HELETFP*CHNMPLLFYRDRLSASD MLQVRKVMDHVYESIITLNNESQST SSSNNEHPGGQERSLARA

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5021	10518	A	5332	2	442	VFMDADTLVLANIDDLFDREELSA APDPGWPDCFNSGVFVYQPSVETY NQLLHLASEQGGDQGILNTFFSSWA TTDIRKHLPFIYNLSSISIYSYLPAI*S EDVSGAISHLVPLGGDSQAMAQAV LVFLGKEPGRGTEWGNKGPRA
5022	10519	A	5333	1	292	VLANIDDLLTREEMSAAQTQGWPD C/FNSGVFVYQPSVET/YNQLLHLAS EQGSFDGGDQGILNTFFSSWATTDI RKHLPFIYNLSSISIYSYLPVLPE
5023	10520	A	5334	81	1163	VTNLRLPRPPAHFVITMTDQAFVTL TTNDAYAKGALVLGSSLKQHRTTR RLVVLATPQVSDSMRKVLETVFDE VIMVDVLDSGDSAHLTLMKRPELG VTLTKLHCWS\LTQYSKCVFMDAD TL\VLANIDD\LFDRE\ELSAAP\DPG G\PDCFNSG\VF\VYQPSV\ETYNQLL HLAS\EQGSFDGG\DQGILNTFF*QL GQQQDIRKHLAF\IYNLSNISIYSYLP AFKVFGASAKVVHFLG\RVKPWNY TY\DPKTKSVK\SEAHDPNMTHPEFL I\LWVGTSFTTNVLPLL\QQFGPWSK DT\CSYVN\VGRCLQGAISHLSLGE\I PA\MAQPF\VSSEERKERWEQGQAD YMGADSFDNIKRKLDTYLQ
5024	10521	A	5335	1	241	GTSNSEHALDDRSTAQCRVQMQVV QQL*LQLAKDKERLQAMMTHLHV KSTEPKAAPQPLNLVSSVTLSKSAL EAYALELT
5025	10522	A	5336	13	229	ACPRSPPPDPRLGCCFPPPPAVC*AP AGPHPDGTTSLECTPAPHPSCEPVS VQQKPEPSALYGTGFPFGLQS
5026	10523	A	5337	1	341	GLGSGTSSSSVKSSISPKRVARWSFS SRVCPVCPSSALSV*DSRSP*ASKSS SNASGSPFCRVKKLLSCELQSKADS FSSSSAVSRDRLSSSSSMLSRGQL*Q ETSKEAQMPR
5027	10524	A	5338	3	168	
5028	10525	B	5339	978	1502	MSNLTLVCISTKHTPGISRAKEKKK GTSRLPTSLCQRRVGLTEEKSCSPEL QQKFRSETITEEELVGLMNKFVEDT KKGVHQKEGWPSSAYGVTKIGVTV LSRIHARKLSEQRKGDKILLNACCP GWVRTDMAGPKATKSPEEGAETPV YLALLPPDAEGPHGQFVSEKRVEQ W*
5029	10526	A	5340	3	239	HEAKSSPNLVKAIILQIQEATQIPRRI NKNKSTLRHIRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLESESMGT
5030	10527	A	5341	3	322	HEAKSSPNLVKAIILQIQEATQIPRRI NKNKSTLRHIRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLSSETMEAR KKWHNYQMIIEKNCQPTILHPAKLS FK
5031	10528	A	5342	4	351	VGRGRQSHLSHSHPPTDPKGQQASP GWNPGVRMLPGLKWLPQPPAASLS *VPSSPTQQTSAGHLLSMSHEALTW

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						VDRATGLAGNGEACVSGTQRHPGL SLAPPGCAPSPSSRAARA
5032	10529	A	5343	3	163	HEEQPEGLSPNLDRFLGDRHCNQFS SRD*PIFLARCSHEYSGRHPRLADSI LL
5033	10530	A	5344	112	362	EREQRFTGLNDVHYLPIMYIVVGCA IFIT*V*RGWSSPTKCRSTDTYCVNP STRLHAYMAPRHKLHSHCAERDPD QFTLLRHC
5034	10531	B	5345	85	206	XFSDPEVKKETRPALGSTVLLAPFL HEHEPPSAEVLPGSWRX*
5035	10532	A	5346	142	653	GFWHQRILGASDQAHLLLPHKQDG SADGARRVLACARGQGDLRLLRLH LAAVPLQLPGGLRRRAVHVHGGGC QQDGGAESWS/PSPSSPRGPRTLHR VEKV\PGAPVTPLPVAFSCNPDHGIE DPAFP*PAAGPR*LQEGPCGGSRAS RAPTPTSTRSCCTECLRNSLILIC
5036	10533	A	5347	261	538	GSRSRLLFSPRGPRTYPAWKRSTGA PVTPSPIAFSCNPDHGIEDPAFP*PAA GPR*LQEGPCGGSRASRAPTPTSTRS CCTKCLRNFLILIC
5037	10534	A	5348	7	264	FQKISALPQRSDYTHNTPHTDPARV SYKHAGANHTHIHTPMTNVSTTIYP PHAYLHTHTQKTPPHIYSTHAP*I*L FISTYAHTKN
5038	10535	A	5349	208	713	SVKMVRYSLDPENPTKSCKSRGS\N LRVHFKNTRETAQAIKGMHI\RKAT\ KYLKDVTLQKQCVPFRRYNGGI\GR CAQAKHWGWTQGR\WP*RVLNSL VIEHIQVNKAPKMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVPKPEEE VAQKKKISQKKLKKQKLMARE
5039	10536	C	5350	286	591	MVRLFNLNPEKRQRKSWQIRGFQS SCFTLGTLVKLAQAIKGMHIRKATE VSERWSLYRNSVYHSDGNNGGVG RRAQAKQWGLGHKVGGPKKECLN FLLHML*
5040	10537	A	5351	1	305	GTSIYNVLYEVPLPPPGRSLKFSGVY GPIICQRPSTNELPLFDFPVKEVFELL GVDNVYQLFTWALLQKYILLYVQR *CNVTKALELSNLLLFHICDIKLV
5041	10538	A	5352	15	234	LSCPDQVHPHSLVPYPEPRRATASV PETSGPPFPHPRRPYATTPPALGHNP HA*LSSSFAGSRYKLGEMLHI
5042	10539	A	5353	3	257	HEVKYKNPAQ*QWHRLGPDAHVPE EFRYHKQLIQSQLFLHYHLSQTFTL QESADLQNAFLNSGQCILNKPLKFA DLHSDFMKTI
5043	10540	A	5354	3	334	IIKFIWNPKRA*IAEAILSKKNIAGGI TLPDFRLYNKAIVI*TAWYWHKNR HIDQWNRILNPEIKSHTYSQRIFDKI DKNIH*GKDTLFNKWCWERWIAIC RRIKLDSLV
5044	10541	A	5355	1	119	QKSRW*TPPNSYMKVNVPEKSRNG ETSLRTKIAVCQYYM
5045	10542	A	5356	3	349	HEPANADFAFRFYYLIASETPGKNIF

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						FSPPRFPAAYAMLSLGACSHSRSQIL EGLGFNLTELSESDARRRCRQ*VGT LDLTGHGLQTRGGQGPWPRARPSR GGDAAAGSARLPPR
5046	10543	A	5357	1	499	
5047	10544	B	5358	66	641	MASKINTKALQSPKRPRSPGSNSKV PEIEVTVEGPNNNNPQTSAVRTPTQ TNGSNVPFKPRGREFSFEAWNAKIT DLKQKVENLFNEKCGEALGLKQAV KVPFALFESFPEDFYVEGLPEGVPFR RPSTFGIPRLEKILRNKAKIKFIIKKP EMFETAIKESTSSKSPPRKINSSPNV NTTASGVEDLNIIQ*
5048	10545	A	5359	2	306	ARGVCGGCRCLGFCGSVVGDLMY* NSFDCFKKVLRY*GFFGLYWGLIP* LIWFAPEQAIYLTDNVFVRDKFT*R DGSDSLSAEVLAGGCALGSLVIVTN SL
5049	10546	A	5360	3	120	HEGKEPDIPLYETVQTVGPSHARTY TVASHSEGR*TIC
5050	10547	A	5361	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAPFLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL S\LQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
5051	10548	A	5362	1	108	
5052	10549	A	5363	2	536	ARAARDWKNYSTDVEAAVNSLVN LYLQASYTYLSLGFYFDRDDVALE GVSHFFRELAEEKREGYERLLKMQ NQRGGRA\LFQDIKKPAEDEWGKTP DAMK\AAMALEKKLNQALLDLHAL GSARTDPHL\CDFLEPHFIDEEVKLI KKMGDHLSNLHRAGWPRRLGLGE YLFERLTLKHD
5053	10550	A	5364	3	331	HEQYPGSISISLTDLGCPDMPVIIAR* TAAADESLVPTRLMLQLADYGPVI YSLVI*VCLTAAFTLAQQHSKMEIY ADIIGSEDTTNEDYRSIALYFEREMR YLQAAKF
5054	10551	A	5365	3	52	HEQSWKAENEAFTLADLKQLPELN PPVLMPRGNVGTPLRVFLELIRACR LPPRIITQLHFQIPKIGYSLRYCNVPF EYEDSDTAVQE*LT
5055	10552	A	5366	3	323	STFFFFFLRQSLALVAQAGLRT\QW RNLGSLQAPPPGFTPFSCLSLPSSWD YRRPPPRLA\NFFFFFFFVFLAETGFH CVLARMVSIS*PRDQPASASQSAGIT GVSD
5056	10553	A	5367	3	337	HERHEDTLTLKERNRGNKGILDDID DHNIIIYHLPDA*SEEYEYFKEQTTL LRASIPFSVGGSNQLIEAIGKMVRGR LYPWSDVKVENPQHNDFMKLITML ITHMHDLQDV
5057	10554	A	5368	16	313	SHSVTQAGVQCWHRLHAQLIFLYF LVETGFHRVSQDGLYLLTS*SARLG LPKCWDYRRDDHAWPVQFFFKCST PRPQAILDFAFTSHELCLGSMRLLKS

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5058	10555	A	5369	1665	1787	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5059	10556	A	5370	1431	1553	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5060	10557	A	5371	1740	1862	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5061	10558	A	5372	1173	1295	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5062	10559	A	5373	1027	1149	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5063	10560	A	5374	2250	2372	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5064	10561	A	5375	934	1092	FFVFLVETGFHRVSQDGLDLLTS*S ARLSLPKCWDYRREPPCPPRIYILTR SR
5065	10562	A	5376	2588	2824	VAGTIGACHHAQLIFVFLVETGFHH VGQDGLDLLTS*STHLGLPKCWDS RREPLRPASPVVFQRTSAPVMADLT PTVS
5066	10563	A	5377	935	1138	RRGFTMFHHVSQGGLDLLTS*SARL GLPKCWDYRREPLCPAWKDY*CKL QDEVISQQGLKVSVVLIH
5067	10564	B	5378	79	1551	MSEVTKNSLEKILPQLKCHFTWNLF KEDSVSRDLEDRVCNQIEFLNTEFK ATMYNLLAYIKHLDGNNEAALECL RQAEELIQQEHADQAEIRSLVTWGN YAWVYYHLGRLSDAQIYVDKVKQ TCKKFSNPYSIEYSELDCEEGWTQL KCGRNERAKVCFEKALEEKPNNPE FSSGLAIAMYHLDNHPEKQFSTDVL KQAIELSPDNQYVKVLLGLKLQKM NKEAEGEQFVEEALEKSPCQTDVLR SAAKFYRRKGDLDKAIELFQRVLES TPNNGYLYHQIGCCYKAKVRQMQ NTGESEASGNKEMIEALKQYAMDY SNKALEKGLNPLNAYSDLAEFLETE CYQTPFNKEVPDAEKQQSHQRYCN LQKYNGKSEDTAVQHGLEGLSISK KSTDKEEIKDQPQNVSENLLPQNAP NYWYLQGLIHKQNGDLLQAAKCY EKELGRLLRDAPSGIGSIFLSASELE DGSEEMGQGAVSSSPRELLSNSEQL N*
5068	10565	A	5379	925	1127	FFVFLVETGFHRVSQDGLDLLTL*S THLGLPKCWDYRREPLRPATFSSYQ RNNPDLILNDTIMPNIK
5069	10566	A	5380	438	815	TRPSFSFNPLTLFFFFLRRSLALSPRL ECSGAISAHCKLRLLGSSHSPTSASR VAGTTSARHHAWLMFFFVFLVETG FHLVSQDSLDLLTS*SAPLGLPKCW DYRHEPPRPAHLHFLNFFLFSYT
5070	10567	A	5381	7944	10115	KQCNYGHNLKTCSNFFFFWRWSLA PSPRLECNGAISAHCKLRPPGFTPFS CLSLPSSWDYRRSPPRAANFFVFLV ETGFHQVSQDGLDLLTL*SARLGLP KCWDYRREPPCPESALIF
5071	10568	A	5382	1	211	LKTSEKWRNRQDKSNKGSKKAEKR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RATHADRNREAARIRRKTYTNERK HYEHHRTAGKDQDERATEDSRE*S RE
5072	10569	A	5383	2	373	ARECHHLCKINYMDLVKEFMTLNA SAPLRSSFSDTMIRLPALTYPLFPAL ATCAGYSDKA*SSISYVLHNSALWR ASGPTDHRDAPA*A*LESRRSTLRIC ELRTLYSLIKSTASNFDPIKLFS
5073	10570	A	5384	112	913	DFLSMPNRRGGVSLPPTPP*PPFSVT HTIFSVSFSFHWLKGSFLRRQFSYCF YGMVLVPFPSHPPLSLSAPSKCLRIP PLPWGWVTAPRLRSHPSVTGRAVL ERKPSVRG*AGSLNTQARDTPPQLP ERPPEG*ALFPPFPYSMAPPSQLKPT LKITAVRS*ASGGATGLGGWSPLGL P*EQGLRPTATLTQTSGIALNPRSLT PAPQLRLSCPPHFALTTRAVPGGPQ PLAWGPEPGTPPAQPRPSPDSAQSH TVYRRESILFFIL
5074	10571	A	5385	2	345	SFWLLCGSSCSDLRSCQVLKCTRNI PYSLVPTASCEHLHGPCIYRPCSVQS VLTCTAAQATNILSAQSLLSGPTTQ* WGLTYPCLLVGAADLTPPTTPPPPT PAPPHLPSTPPP
5075	10572	B	5386	36	340	MFLDEYARRHPDYSVVLLLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCELFEQLGEY KFQNALLVRYTKKNALCRRLSIRGP EPVI*
5076	10573	A	5387	3	182	
5077	10574	C	5388	602	877	METTLRRKCCARLQILHGMAMPKV FRWNFKPLVGRSLRNLNPNKIVEAF WSQLGRSYKFPGMRYLVSFTPKES YPKCSNFPTLCRRVFKET*
5078	10575	A	5389	1	404	GTRNDKMEPGLEQGTIPRLDSVTSS ECFASSGFHEDRSLSDVEEQEDSDG FYKEPITMEDLISYSFQVAIGMESLS SRLCIHRDLEARNFHLSGNYCDTSL EF*IENYDIYL**FNIYSPTKLKPEDT RLLKET
5079	10576	A	5390	110	424	LSLLQREREGHLNGSPSFMLKCSGF YRLA*GVCV*VSFVL*Y*HILIYSML TVLILCIYFFNMLISGIYTDYAYFYIC YIYYYCYIF*FILLCFYTLMTIFFGLI
5080	10577	A	5391	2	361	ARETVKRIQYPIPLEGRLGLKPLIES LI*DGLLELCMSPYTTPILLVK*SDW *Y*LVEDLQAINQTVQTTHPVVPNP YTILSKIPYDHQWFTEIDLKDAFWA CPLAEDS*DIFTFEWARA
5081	10578	A	5392	3	335	QSQSWWRQKGVSRAGAGPIHPQGL LFGFS*GDLGPLGTLGEQGLIGQRG EPGLEGDSGPMGPDGLKGVRGDPG PDGEHGEKGQEGLMGEDGPPGPPG AAGVRGLHGKSGY
5082	10579	A	5393	61	497	
5083	10580	A	5394	16	951	RRPKIRDKFWGSV/KKLAHSEASPVI SGASKRAKKQINVYVGKGSS/QGK

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						MVVWVKKLDRDTVFALVNYIFFKG KWERPFEVKDTEEEDFHVDQATTV KVPMMKRLGMFNIQHCKKLSSWV LLMKYLGNATAIFFLPDEGKLQHLE N\ELTHD\IVTKFLE\NEDRRSASLHL PKLSITGTYDLK\TVLGQ\LGITKVFS NGAD\LSGVTEEAPLKLSKAVH*GC A*PSTEERGLKLAGGHVF*EGHYPC FIPPRGSSFNKPFVFLNGFEQN/SPSF PLFMGEKWVNPTPKITGLSLLNPSP PSLGPLPGMTLKKGLSWK
.5084	10581	A	5395	2	306	GFDHVAQAGLEPLGSSDLPPSASQS AGITGMSHHTQPAYILKISFITLPFIIR SLS*VPFVFSIMYKSSFNFSPCGESVF STNLLNNEYLLIDWWLHFIIY
5085	10582	A	5396	1	375	
5086	10583	A	5397	162	426	
5087	10584	A	5398	140	426	
5088	10585	A	5399	158	705	PSEKNKNNLLLGVVYVRHLPNLLD ETQIFSYFSQFG\PVTRFRLSR\NKRT GN\SKGYAF\LEFESEDVCQNSCLKQ WNNYLFGGKTLG/QCHFMPPEKVH K\NSFKDWDFPFKQPSYPSVKRV*S ESDTNTKA/DGMEERFKKKERLLRK KLAKKGIDYDFPSLILQKTESISKTN RQTSTKGQVFT
5089	10586	A	5400	2	388	FLFFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA
5090	10587	C	5401	197	415	MLLYVGLEPHHTHMLSLWPPRLMF PSVFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASAF*
5091	10588	A	5402	671	986	KGVLFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5092	10589	A	5403	65	921	
5093	10590	A	5404	213	442	
5094	10591	A	5405	1	1506	
5095	10592	A	5406	1	286	DRLIYIPFPDEKSLVPILKANLGKSP\ VPKDLDLEFLDLVPWGCGRLPRRG NQGCAHSLLHSPAGHACYSLTLDR GFLLQKSKPKAVKLPRFSFG
5096	10593	A	5407	2	158	
5097	10594	A	5408	1	9064	MLARAARGTGALLLRGSLLASGRA PRRASSGLPRNTVVLFVPQQEAWV VERMGRFHRILEPGLNILIPVLDRIR YVQSLKEIVINVPEQSAVTLDNVTL QIDGVLYLRIMDPYKASYGVEDPEY AVTQLAQTTMRSELGKLSLDKVFR ERESLNASIVDAINQAADCWGIRCL RYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QAQILASEAEKAEQINQAAGEASAV LAKAKAKAEAIRILAAALTQHNGD AAASLTVAEQYVSAFSKLAKDSNTI LLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTDAS LDEELDRVKMTWSPVPNFQLLNIPS NWGQPHAPGQTSTEVPADGDGATD GPLCLAHASLCCQVAGAAAAALPG AIAGGAVGWARIPLRLRSLSTGMQ KASVLLFLAWVCFLFYAGIALFTSG FLLTRLELTNHSSCQEPPGPGSLPW GSQGKPGACWMASRFSRVVLVLID ALRFDFAQPQHSHVPREPPVSLPFL GKLSSLQRILEIQPHHARLYRSQVDP PTTTMQRLKALTTGSLPTFIDAGSN FASHAIVEDNLIKQLTSAGRRVVFM GDDTWKDLFPGAFSKAFFFPSFNVR DLDTVDNGILEHLYPTMDSGEWDV LIAHFLGVDHCGHKHGPHHPEMAK KLSQMDQVIQGLVERLENDTLLVV AGDHGMTTNGDHGGDSELEVSAA LFLYSPTAVFPSTPPEEPEVIPQVSLV PTLALLLGLPIPFGNIGEVMAELFSG GEDSQPHSSALAQASALHLNAQQV SRFLHTYSAATQDLQAKELHQLQN LFSKASADYQWLLQSPKGAEATLP TVIAELQQFLRGARAMCIESWARFS LVRMAGGTALLAASCFICLLASQW AISPGFPFCPLLLTPVAWGLVGAIAY AGLLGTIELKLDLVLLGAVAAVSSF LPFLWKAWAGWGSKRPLATLFPIP GPVLLLLLFRLAVFFSDSFVVAEAR ATPFLLGSFILLLVVQLHWEGQLLP PKLLTMPRLGTSATTNPPRHNGAY ALRLGIGLLLCTRLAGLFHRCPEETP VCHSSPWLSPLASMVGGRAKNLW YGACVAALVALLAAVRLWLRRYG NLKSPEPPMLFVRWGLPLMALGTA AYWALASGADEAPPRLRVLVSGAS MVLPRAVAGLAASGLALLLWKPVT VLVKAGAGAPRTRTVLTPFSGPPTS QADLDYVVPQIYRHMQEEFRGRLE RTKSQGPLTVAAYQLGSVYSAAMV TALTLLAFPLLLLHAERISLVFLLLF LQSFLLLHLLAAGIPVTTPGKYLSSD SLKDNSDSQGLRKRQQPPGNEADA RVRPEEEEPLMEMRLRDAPQHFY AALLQLGLKYLFILGIQILACALAAS ILRRHLMVWKVFAPKFIFEAVGFIV SSVGLLLGIALVMRVDGAVLLSSAS TERHCQQTTRGRKPTLVSVLVLDSE QRKDGRLRSALVSSYRFLETPSAGA ELFRPASATMSRQTTSVGSSCLDLW REKNDRLVRQAKVAQNSGLTLRRQ QLAQDALEGLRGLLHSLQGLPAAV PVLPLELTVTCNFIILRASLAQGFTE DQAQDIQRSLERVLETQEQQGPRLE QGLRELWDSVLRASCLLPELLSALH

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RLVGLQAALWLSADRLGDLALLLE TLNGSQSGASKDLLLLLKTWSPPAE ELDAPLTLQDAQGLKDVLLTAFAY RQGLQELITGNPDKALSSLHEAASG LCPRPVLVQVYTALGSCHRKMGNP QRALLYLVAALKEGSAWGPPLLEA SRLYQQLGDTTAELESLELLVEALN VPCSSKAPQFLIEVELLLPPPDLASP LHCGTQSQTKHILASRCLQTGRAGD AAEHYLDLLALLLDSSEPRVGPCMP EVFLEAAVALIQAGRAQDALTLCEE LLSRTSSLLPKMSRLWEDARKGTKE LPYCPLWVSATHLLQGQAWVQLG AQKVAISEFSRCLELLFRATPEEKEQ GAAFNCEQGCKSDAALQQLRAAAL ISRGLEWVASGQDTKALQDFLLSV QMCPVSAKRLRPSFESSLPLPLPL PPRGSGASVVRPTPRCRPRPARLAP LERTSGPGQVFRPTPPGRRPGALGR QSAVRPTTRRKPLVPGESRPREPEA PAGPEEDIKVQRLGNLPKITIKQWH NWNSDPMGLTIEFLLLTTLLSKGDD LSTAILKQKNRPNRLIVDEAINEDNS VVSLSQPKMDELQLFRGDTVLLKG KKRREAVCIVLSDDTCSDEKIRMNR VVRNNLRVRLGDVISIQPCPDVKYG KRIHVLPIDDTVEGITGNLFEVYLKP YFLEAYRPIRKGDIFLVRGGMRAVE FKVVETDPSPYCIVAPDTVIHCEGEP IKREDEEESLNEVGYDDIGGCRKQL AQIKEMVELPLRHPALFKAIGVKPP RGILLYGPPGTGKTLIARAVANETG AFFFLINGPEIMSKLAGESESNLRKA FEEAEKNAPAIIFIDELDAIAPKREKT HGEVERRIVSQLLTLMDGLKQRAH VIVMAATNRPNSIDPALRRFGRFDR EVDIGIPDATGRLEILQIHTKNMKLA DDVDLEQVANETHGHVGADLAAL CSEAALQAIRKKMDLIDLEDETIDA EVMNSLAVTMDDFRVRTTPVPQW ALSQSNPSALRETVVEVPQVTWEDI GGLEDVKRELQELVQYPVEHPDKF LKFGMTPSKGVLFYGPPGCGKTLL AKAIANECQANFISIKGPELLTMWF GESEANVREIFDKARQAAPCVLFFD ELDSIAKARGGNIGDGGGAADRVIN QILTEMDGMSTKKNVFIIGATNRPDI IDPAILRPGRLDQLIYIPLPDEKSRVA ILKANLRKSPVAKAGARSWADV\D LGVPGLKMTNGFSGS*P*QEILPACF AKLAI\RESNREVKIKAKNREEGKT NPIKPMGRYE*WIDPVP\EIR\RDSLL KEAQSFCAPFLFSDNDIR\KY\EMFA QTLSQ/ESRGFGSRFPSGNQGGAGP SQGSGGGTGGSVYTEDNDDDLYG
5098	10595	A	5409	96	299	
5099	10596	A	5410	174	324	
5100	10597	A	5411	74	242	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5101	10598	A	5412	129	899	AAPGLGRGGGAAAGGGAVCPGTE RPCAMAYAYLFKYIIGRTTGVG*N PCPNALQFTD/KRGFQPSAMTLTIGV EFGA\RMITIDGKQIKL\QIWDTAGQ ESFRS\ITRSYYRGAAGALLVYDITR\ *DTFNH\LTTW\LEDARQHSNSNM\V IMLIG\NKSD\LESRREVKKE/EKGEA FA\REHGLIFM\ETSAKTGFQCRKEG ILFNTAKEILLKKFPRKGVFLTFN*W RANGH/IKLGPQPAAYPIATHAGQS G\GQQAGGGCC
5102	10599	A	5413	1	408	MQLKRANPGPRRAPVRETVMLLLC WGVPPGRPYKVDTESALLYQGPHN TLFGYSVVLHSHGANR\WGAPTAN WLANASVINPGAIYRCRIGKNPGQT CEQLQLGSPNGEPCGKTCLEERDNQ WLGVTLSRQPGENG
5103	10600	C	5414	1	1026	MGLGIYLDQYTRQKGQDPVAELKQ LIPLVVSLSAPNLEMPLLKKKTTNPS TFLKSLSGGLNLFNFPFVETYTVEE VKVHPRNNTGGYNPEEEEDETASE NCFPWNVDGDLMEVASEVHIRRVQ KKEYVEENKIPRNPTYKGCEGPLQE NYKPLLNKIKEDTNKWKNIPCSWIG RTDTVKMAILPKHDRVAEQRVVGA LVKQRASQCPRCRGGRSGPPGTAT ASPSPGRRPFGAVIAPRFPSHALSSW YAGCNAEKSEVNAFPGTQGMRFIS AASYKDWVQVLQQKDVSRNMGTK ARMMPLGSSGGCHTIRTEVTQDSE GQLAAVTTTGYTVVGLEPPKVSD*
5104	10601	A	5415	1	681	
5105	10602	A	5416	1	779	MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEEK VPETTTRFWAPGVEAPGDDAERRR REASGPATRHSPLPTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQEESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF
5106	10603	A	5417	1	1274	MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPGPLGLLGV RPGMPPQPQGPAPLRRPDSSDDRYV MTKHATIYPTEEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAII LNSCVEPKMQVTITLTSPIIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCVIIR ILRDLCQRVP\TWS\DFPSWAMELLV EKAISSAS\SPQSPGDAL\RRVF\ECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PD\QQR\EDITSSAQFA\LRLLAF\

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RQIHKVLGMDPLPQMS\QRFN\IHNH QDR\RRDSDGVDGFEAEGKKDKKD YDNF
5107	10604	A	5418	144	522	VDLLRAAGRQWQGPLRPRPSGRR* SARRA/LGKTTYCTDPAKFISVLWT YLATMLHVELPHMNLLSTMDLIEH YGKLAFNLDYYTEVLDLS*LLDHL AS/VPFLTAYRQVTEKLVQLIEDYIL RCFIHP
5108	10605	A	5419	1	2437	MAVPGEAEEEATVYLVVSGIPSVLR SAHLRSYFSQFREERGGGFLCFHYR HRPERAPPQAAPNSALIPTDPAAEG QLLSQTSATDVRPLSTRDSTPIQTRT CCCVISVRGLAQAQRLIRMYSGRR WLDSHGTWLPGRCLIRRLRLPTEAS GLGSFPFKTRKELQSWKAENEAFTL ADLKQLPELNPPVLMPRGNVGTPL RVFLELIRACRLPPRIITQLQLQFPKT GSSRRYGNVPFEYEDSETVEQEELV YTAEGEEIPQGTYLADIPASPCGEPE EEVGKEEEEESHSDEDDDRGEEWE RHEALHEDVTGQERTTEQLFEEEIE LKWEKGGSGLVFYTDAQFWQEEE GDFDEQTADDWDVDMSVYYDRDG GDKDARDSVQMRLEQRLRDGQED GSVIERQVGTFERHTKGIGRKVMER QGWAEGQGLGCRCSGVPEALDSDG QHPRCKRGLGYHGEKLQPFGQLKR PRRNGLGLISTIYDEPLPQDQTESLL RRQPPTSMKFRTDMAFAVIGPPGSG KTTYCLGMSEFLRALGRRVAVVNL DPANEGLPYECAVDVGELVGLGDV MDALRLGPNGGLLYCMEYLEANL DWLRAKLDPLRGHYFLFDCPGQVE LCTHHGALRSIFSQMAQWDLRLTA VHLVDSHYCTDPAKFISVLCTSLAT MLHVELPHINLLSKMDLIEHYGKLA FNL\DYYTEVLDLSYLL*PPGLLTLS SATTRPASIEEA/MCKLIEDY\NLVSF IPLNIQDKESIQRVLQAVDKANGYC FGAQEQRSLEAMMSAAMGADFHFS STLGIQEKYLAPSNQSVEQEAMQL
5109	10606	A	5420	2	78	
5110	10607	A	5421	94	253	
5111	10608	A	5422	2	318	
5112	10609	A	5423	460	672	
5113	10610	A	5424	357	795	
5114	10611	A	5425	310	478	
5115	10612	A	5426	1	399	
5116	10613	A	5427	2	390	
5117	10614	A	5428	3	392	GGKIIVGDATEKDASKKSDSNP\LTE ILKCPTKVVLLRNMVGAGEVDEDL EVETKEECEK\YGKVGKCVI\FEIPG APDDEAVRIFLEFERVE\SAIKAVVD LNGRYFGGRVVKACFYNLDKFRVL DLAEQV
5118	10615	A	5429	837	1005	

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5119	10616	A	5430	174	247	
5120	10617	A	5431	1	360	
5121	10618	A	5432	1	382	
5122	10619	A	5433	338	442	
5123	10620	A	5434	1	140	
5124	10621	A	5435	3	339	PINFESVGPTYRGSSCLAVVVPEFLG MSVAFVPDWLRGKAEVNQETIQR\L LE*NDQLIRCI\LEYQNKARGNECVQ YQHVLHRNLI\YLATIADAQSQPALS KAMGIIFQKQ
5125	10622	A	5437	157	371	
5126	10623	A	5438	150	284	
5127	10624	A	5439	84	901	ARKSVRMASSRMTRRDPLTNKVAL VTASTDGIGFAIARRLAQDRAHVVV SSRKQQNVDQ\AVATL\QGEGLSVT GTVCHVGKAEDRGAAWWPPAVKL HGGIDILVSNAAVNPFFGSIMDVTE EV\WDKTLDI\NVKGPKP*MTKAVV PEMEKRGGGS\VVIVSSIAAFSPSPG FSPYNVSKTALLGLAQT\LPIEL\APR NIRV\NCLAPG\LIKTSF\SRMLW\MD KEKEESMKETLR\IRRLGEPEDCAGI VSFLCSEDASYITGETVVVG\GGTPS RL
5128	10625	A	5440	2	468	
5129	10626	A	5441	63	219	
5130	10627	A	5442	3	558	
5131	10628	A	5443	7	909	DQCEVCRNSEVRPAACPGHSGSPA QGPPRPFRMKAAVLTLAVLFLTGSQ ARHFWQQDEPPQSPWDRVKDLAT VYVDVLKDSGRDYVSQFEGSALGK QLNLKLLDNWDSVTSTF\SKLREQL GPVTQEFWDNLEKETEGLRQEMSK DLEEVKAKVQPYL\DDFQKKW\QEE MELYRQKVEPLRAELQEGARQKLH ELQEKLSPLGEEMRDRARA\HVDAL RTHLAPYSGELRQRLGAR\LGALRE NGGARMGQYHA\QATEHLSTLSEK AKPALEDLRQGLLPVLESFKVSFLS ALEEYTKKLNTQ
5132	10629	A	5444	3	195	
5133	10630	A	5445	189	263	PPGSHLGHPANAPSH*GPYPGLHS
5134	10631	A	5446	1905	2052	
5135	10632	A	5447	1903	2050	
5136	10633	A	5448	1	115	
5137	10634	A	5449	1	402	GKTSKLEFSIYLAPHSTTAAIEPYNSI LTTHTTLEHYDWAFMAYNGAIYDI CRRNLDIGRTTYTNLNTLIGQIESSIT ASLRFDGALNGDLT*FQTNLVPYPR IHFPLATYAPVISAEKAYHEQLSVA EITNAC
5138	10635	B	5450	81	319	XVVEPYNSILTTHTTLEHSDCAFMV DNEAIYDICRRNLDIERPTYTNLNRL IGQIVSSITASLRFDGALNVDLTEFQ TNL*
5139	10636	A	5451	1	422	GKKSKLEFSIYPAPQVSTAVVEPYN SILTTHTTLEHSDCAFMVDNEAIYDI

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						CRRNLDIERATYTNLNRIIGQIVSSIT ASLRFDGALNVDLTEFQTNLVPYPR MHLPLGTYAPVICAEK/AYHETAFV QKTTCLG*PSQQMW
5140	10637	A	5452	771	1640	ALQLHPHHPHHPWSTLIVPFMVDN EAIYDICRRNLDIERPTYTNLNRVIR A/QMGPSITASLRFDGA\LNV\DLTEF QTNPGAPTPRIHLP/LWPTYAPVHLL AGGKPYHGTAFL*AGGFTNGLVLE ARPTQMGGNVDPW\HGVNYMGLL AWLYRGDVGFPKIDNGWPLPTIKN QAQHSSFVDW/CGPTGLSRFGHSTY QPSTVVPGLETWAKV\QRAV\CML\ SNTTAIAE\A*ARLDHKFDLMYAKR AF\VHWYVGEGMKEGEFSEAREDM AALEKDYEEVGVDSVEGEGEEEGE EY
5141	10638	A	5453	89	435	
5142	10639	A	5454	2	287	TNEIEPEEN*HTKARNFRRFVTAINN TPRNIRED/GDHLLHHWIALLADCPI TAHMYEDVALIKDHTLDNSLIRELQ TLQEFNITLETALVKGIDI
5143	10640	B	5455	218	3940	MSGGGGGGGSAPSRFADYFVICGL DTETGLEPDELSALCQYIQASKARD GASPFISSTTEGENFEQTPLRRTFKS KVLARYPENVEWNPFDQDAVGML CMPKGLAFKTQADPREPQFHAFIIT REDGSRTFGFALTFYEEVTSKQICSA MQTLYHMHNAEYDVLHAPPADDR DQSSMEDGEDTPVTKLQRFNSYDIS RDTLYVSKCICLITPMSFMKACRSV LQQLHQAVTSPQPPPLPLESYIYNVL YEVPLPPPGRSLKFSGVYGPIICQRP STNELPLFDFPVKEVFELLGVENVF QLFTCALLEFQILLYSQHYQRLMTV AETITALMFPFQWQHVYVPILPASL LHFLDAPVPYLMGLHSNGLDDRSK LELPQEANLCFVDIDNHFIELPEDLP QFPNKLEFVQEVSEILMAFGIPPEGN LHCSESASKLKRLRASELVSDKRNG NIAGSPLHSYELLKENETIARLQALV KRTGVSLEKLEVREDPSSNKDLKV QCDEEELRIYQLNIQIREVFANRFTQ MFADYEVFVIQPSQDKESWFTNRE QMQNFDKASFLSDQPEPYLPFLSRF LETQMFASFIDNKIMCHDDDDKDP VLRVFDSRVDKIRLLNVRTPTLRTS MYQKCTTVDEAEKAIELRLAKIDHT AIHPHLLDMKIGQGKYEPGFFPKLQ SDVLSTGPASNKWTKRNAPAQWRR KDRQKQHTEHLRLDNDQREKYIQE ARTMGSTIRQPKLSNLSPSVIAQTN WKFVEGLLKECRNKTKRMLVEKM GREAVELGHGEVNITGVEENTLIAS LCDLLERIWSHGLQVKQGKSALWS HLLHYQDNRQRKLTSGSLSTSGILL DSERRKSDASSLMPPLRISLIQDMR HIQNIGEIKTDVGKARAWVRLSME

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KKLLSRHLKQLLSDHELTKKLYKR YAFLRCDDEKEQFLYHLLSFNAVD YFCFTNVFTTILIPYHILIVPSKKLGG SMFTANPWICISGELGETQIMQIPRN VLEMTFECQNLGKLTTVQIGHDNS GLYAKWLVEYVMVRNEITGHTYKF PCGRWLGKGMDDGSLERILVGELL TSQPEVDERPCRTPPLQQSPSVIRRL VTISPNNKPKLNTGQIQESIGEAVNG IVKHFHKPEKERGSLTLLLCGECGL VSALEQAFQHGFKSPRLFKNVFIWD FLEKAQTYYETLEKNEVVPEENWH TRARNFCRFVTAINNTPRNIGQGWQ VSDAGVLGEPEITSYTTGICPAG*
5144	10641	A	5456	238	406	
5145	10642	A	5457	2	204	
5146	10643	A	5458	1	431	
5147	10644	A	5459	1	225	
5148	10645	A	5460	3	321	
5149	10646	A	5461	1	1257	MSHRKFSAPRHGSLGFLPRKRSSRH RGKVKSFPKDDPSKPVHLTAFLGY KAGMTHIVREVDRPGSKVNKKEVV EAVTIVETPPMVVVGIVGYVETPRG LRTFKTVFAEHISDECKRRFYKNWH KSKKKAFTKYCKKWQDEDGKKQL EKDFSSMKKYCQVIRVIAHTQMRL LPLRQKK\AHLMGDQVERGALWPE KADW\ARER\LEQQVPVNQVF\GQD EMIDVIG\VTQGQKAYKGV\TSRWH TQESCPRKDPTEGLRK\VACIRAW\H PARVAFSVARA\GQ\KGYHHRTEIN K\KIYKIGQGYLIKGG\KLIKNNAST\ DYDL/SLDKSINPSGWAFVHLW*K* PNDFVML\KG\CVVGTKK\RVLTLR KSFAGCRRKRRGFGEELTLSSIDTTS KF\GHGRFQTMEEKKAFMG\PLKKD RIAKEEGA
5150	10647	A	5462	114	456	
5151	10648	A	5463	3	76	
5152	10649	A	5464	2	951	CWNSGEVRWPLPPPPPRFVARRKM ADLEEQLSDEEKVRIF\LKFFIHAPPG EINEGFNDVRLLLNNDNLLREGAA HAFAQYNLDQFTPLKIEG\YEDQVLI TEHGRLGEMGKFL\DPKN\RICFKF* SL*GRRATDPKDPC\EV\ENAVESWR TSVETALRAYVKEHYPEWESGTVY GQKNRWDSQTIIACI\ESHQFQAKNF WNGRWRSEWKFTITPSTTQVVG\IL KIQVHYYEDGNVQLVSHKDIQDSL TVSNEVQTAKEFIKIVEAAENEYQT AISENYQTMSDTTFKALRRQLPVTR TKIDWNKILSYKIGKEMQNA
5153	10650	A	5465	3	553	
5154	10651	B	5466	26	384	MHHEALSEALPGDNVGFNVKNVSV KDVRRGNVAGDSKNDPPMEAAGF TAQVIILNHPGQISAGYALYWIAIVD MVPGKPMCVESFSDYPPLGRFAVR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DMRQTVAVGVIKAVDKKAAGLAS*
5155	10652	A	5467	1	1254	
5156	10653	A	5468	1	1386	
5157	10654	A	5469	33	1653	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLKAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVL\IVAA GVGEFEAG\ISKNGQTREHALLAYT LGVKQ\LIV\GVNKMDSTEPPYSQK RYEEIVKEVSTYIKKIGYY\PDTLAF EPISGWNGDDMLEPSANMPWFKG WKVTRKDG\NAS\GTTLLEAL\DC\IL PPTRPT\DKPLR\LPLQ\DVYKIGGIG\ TVPVG\RVETGVLKPG\MGVTF\APS QRLQREVKICPKMHHEAFE*SSFLG DNVGF\NVKNVSCQGCSVRGNV*H GDSK\NDPPMEA/SLGFTAQVII\LNH PGPNKAPG*CPWYWDCHTAH\IAC KVCLSLKEKI*F/DRSW*KSLEDGP*I LGSLGDAGHWLIWVPGQAPCVFEK LLKTIPP\LGRFA\VRDNEDRQLCGW VSIKSSWTKKAAGSWAKVTK\SAQ KSSERLKWNIIPNTCHPTLYQVWEE RSQELFGSIGHLSLSSKRLVNDNNA S
5158	10655	A	5470	2	4966	
5159	10656	A	5471	2	4821	RWPRRARLLRRGRGGGGVESLPHF GAPVPRARLQLTARRGHAGLRARM REAAAALVPPPAFAVTPAAAMEEPP PPPPPPPPPEPETESEPECCLAARQE GTLGDSACKSPESDLEDFSDETNTE NLYGTSPPSTPRQMKRMSTKHQRN NVGRPASRSNLKEKMNAPNQPPHK DTGKTVENVEEYSYKQEKKIRAAL RTTERDHKKNVQCSFMLDSVGGSL PKKSIPDVDLNKPYLSLGCSNAKLP VSVPMPIARPARQTSRTDCPADRLK FFETLRLLLKLTSVSKKKDREQRGQ ENTSGFWLNRSNELIWLELQAWHA GRTINDQDFFLYTARQAIPDIINEILT FKVDYGSFAFVRDRAGFNGTSVEG QCKATPGTKIVGYSTHHEHLQRQR VSFEQVKRIMELLEYIEALYPSLQAL QKDYEKYAAKDFQDRVQALCLWL NITKDLNQKLRIMGTVLGIKNLSDI GWPVFEIPSPRPSKGNEPEYEGDDT EGELKELESSTDESEEEQISDPRVPEI RQPIDNSFDIQSRDCISKKLERLESE DDSLGWGAPDWSTEAGFSRHCLTSI YRPFVDKALKQMGLRKLILRLHKL MDGSLQRARIALVKNDRPVEFSEFP DPMWGSDYVQLSRTPPSSEEKCSA VSWEELKAMDLPSFEPAFLVLCRVL LNVIHECLKLRLEQRPAGEPSLLSIK QLVRECKEVLKGGLLMKQYYQFM LQEVLEDLEKPDCNIDAFEEDLHKM LMVYFDYMRSWIQMLQQLPQASHS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LKNLLEEEWNFTKEITHYIRGGEAQ AGKLFCDIAGML\LKSTGSFLEFGLQ ESCAEFWTSADDSSASDEIIRSVIEIS RALKELFHEARERASKALGFAKML RKDLEIAAEFRLSAPVRDLLDVLKS KQYVKVQIPGLENLQMFVPDTLAE EKSIILQLLNAAAGKDCSKDSDDVL IDAYLLLTKHGDRARDSEDSWGTW EAQPVKVVPQVETVDTLRSMQVDN LLLVVMQSAHLTIQRKAFQQSIEGL MTLCQEQTSSQPVIAKALQQLKND ALELCNRISNAIDRVDHMFTSEFDA EVDESESVTLQQYYREAMIQGYNF GFEYHKEVVRLMSGEFRQKIGDKYI SFARKWMNYVLTKCESGRGTRPR WATQGFDFLQAIEPAFISALPEDDFL SLQALMNECIGHVIGKPHSPVTGLY LAIHRNSPRPMKVPRCHSDPPNPHLI IPTPEGFRGSSVPENDRLASIAAELQ FRSLSRHSSPTEERDEPAYPRGDSSG STRRSWELRTLISQSKDTASKLGPIE AIQKSVRLFEEKRYREMRRKNIIGQ VCDTPKSYDNVMHVGLRKVTFKW QRGNKIGEGQYGKVYTCISVDTGEL MAMKEIRFQPNDHKTIKETADELKI FEGIKHPNLVRYFGVELHREEMYIF MEYCDEGTLEEVSRLGLQEHVIRLY SKQITIAINVLHEHGIVHRDIKGANIF LTSSGLIKLGDFGCSVKLKNNAQTM PGEVNSTLGTAAYMAPEVITRAKG EGHGRAADIWSLGCVVIEMVTGKR PWHEYEHNFQIMYKVGMGHKPPIP ERLSPEGKDFLSHCLESDPKMRWT ASQLLDHSFVKVCTDEE
5160	10657	A	5472	3	425	
5161	10658	A	5473	1	234	
5162	10659	A	5474	3	260	
5163	10660	A	5475	3255	3467	LNKNLGLIFFFFFFFFFFFETASRSVT\R LEYSGSILAHCELRLPGSRHSPVVSA TWEAEAGELPEPRRQRLR
5164	10661	A	5476	1	4497	
5165	10662	A	5477	2	891	
5166	10663	A	5478	1	9786	
5167	10664	A	5479	27	13959	VPFSVAAAEEPAQPARAARPRPGRS PGAAPPQLAMDPPRPALLALLALPA LLLLLLAGARAEEEMLENVSLVCPK DATRFKHLRKYTYNYEAESSSGVP GTADSRSATRINCKVELEVPQLCSFI LKTSQCILKEVYGFNPEGKALLKKT KNSEEFAAAMSRYELKLAIPEGKQV FLYPEKDEPTYILNIKRGIISALLVPP ETEEAKQVLFLDTVYGNCSTHFTV KTRKGNVATEISTERDLGQCDRFKP IRTGISPLALIKGMTRPLSTLISSSQS CQYTLDAKRKHVAEAICKEQHLFL PFSYKNKYGMVAQVTQTLKLEDTP KINSRFFGEGTKKMGLAFESTKSTS PPKQAEAVLKTVQELKKLTISEQNI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRANLFNKLVTELRGLSDEAVTSLL PQLIEVSSPITLQALVQCGQPQCSTH ILQWLKRVHANPLLIDVVTYLVALI PEPSAQQLREIFNMARDQRSRATLY ALSHAVNNYHKTNPTGTQELLDIA NYLMEQIQDDCTGDEDYTYLILRVI GNMGQTMEQLTPELKSSILKCVQST KPSLMIQKAAIQALRKMEPKDKDQ EVLLQTFLDDASPGDKRLAAYLML MRSPSQADINKIVQILPWEQNEQVK NFVASHIANILNSEELDIQDLKKLVK EVLKESQLPTVMDFRKFSRNYQLY KSVSIPSLDPASAKIEGNLIFDPNNY LPKESMLKTTLTAFGFASADLIEIGL EGKGFEPTLEALFGKQGFFPDSVNK ALYWVNGQVPDGVSKVLVDHFGY TKDDKHEQDMVNGIMLSVEKLIKD LKSKEVPEARAYLRILGEELGFASL HDLQLLGKLLLMGARTLQGIPQMI GEVIRKGSKNDFFLHYIFMENAFEL PTGAGLQLQISSSGVIAPGAKAGVK LEVANMQAELVAKPSVSVEFVTNM GIIIPDFARSGVQMNTNFFHESGLEA HVALKPGKLKFIIPSPKRPVKLLSGG NTLHLVSTTKTEVIPPLIENRQSWSV CKQVFPGLNYCTSGAYSNASSTDSA SYYPLTGDTRLELELRPTGEIEQYSV SATYELQREDRALVDTLKFVTQAE GAKQTEATMTFKYNRQSMTLSSEV QIPDFDVDLGTILRVNDESTEGKTS YRLTLDIQNKKITEVALMGHLSCDT KEERKIKGVISIPRLQAEARSEILAH WSPAKLLLQMDSSATAYGSTVSKR VAWHYDEEKIEFEWNTGTNVDTKK MTSNFPVDLSDYPKSLHMYANRLL DHRVPQTDMTFRHVGSKLIVAMSS WLQKASGSLPYTQTLQDHLNSLKE FNLQNMGLPDFHIPENLFLKSDGRV KYTLNKNSLKIEIPLPFGGKSSRDLK MLETVRTPALHFKSVGFHLPSREFQ VPTFTIPKLYQLQVPLLGVLDLSTN VYSNLYNWSASYSGGNTSTDHFSL RARYHMKADSVVDLLSYNVQGSG ETTYDHKNTFTLSCDGSLRHKFLDS NIKFSHVEKLGNNPVSKGLLIFDASS SWGPQMSASVHLDSKKKQHLFVKE VKIDGQFRVSSFYAKGTYGLSCQRD PNTGRLNGESNLRFNSSYLQGTNQI TGRYEDGTLSLTSTSDLQSGIIKNTA SLKYENYELTLKSDTNGKYKNFAT SNKMDMTFSKQNALLRSEYQADYE SLRFFSLLSGSLNSHGLELNADILGT DKINSGAHKATLRIGQDGISTSATT NLKCSLLVLENELNAELGLSGASM KLTTNGRFREHNAKFSLDGKAALT ELSLGSAYQAMILGVDSKNIFNFKV SQEGLKLSNDMMGSYAEMKFDHT NSLNIAGLSLDFSSKLDNIYSSDKFY

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SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KQTVNLQLQPYSLVTTLNSDLKYN ALDLTNNGKLRLEPLKLHVAGNLK GAYQNNEIKHIYAISSAALSASYKA DTVAKVQGVEFSHRLNTDIAGLAS AIDMSTNYNSDSLHFSNVFRSVMAP FTMTIDAHTNGNGKLALWGEHTGQ LYSKFLLKAEPLAFTFSHDYKGSTS HHLVSRKSISAALEHKVSALLTPAE QTGTWKLKTQFNNNEYSQDLDAY NTKDKIGVELTGRTLADLTLLDSPI KVPLLLSEPINIIDALEMRDAVEKPQ EFTIVAFVKYDKNQDVHSINLPFFET LQEYFERNRQTIIVVLENVQRNLKH INIDQFVRKYRAALGKLPQQANDY LNSFNWERQVSHAKEKLTALTKKY RITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANI IDEIIEKLKSLDEHYHIRVNLVKTIH DLHLFIENIDFNKSGSSTASWIQNVD TKYQIRIQIQEKLQQLKRHIQNIDIQ HLAGKLKQHIEAIDVRVLLDQLGTT ISFERINDVLEHVKHFVINLIGDFEV AEKINAFRAKVHELIERYEVDQQIQ VLMDKLVELAHQYKLKETIQKLSN VLQQVKIKDYFEKLVGFIDDAVKK LNELSFKTFIEDVNKFLDMLIKKLKS FDYHQFVDETNDKIREVTQRLNGEI QALELPQKAEALKLFLEETKATVA VYLESLQDTKITLIINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDI QQELQRYLSLVGQVYSTLVTYISD WWTLAAKNLTDFAEQYSIQDWAK RMKALVEQGFTVPEIKTILGTMPAF EVSLQALQKATFQTPDFIVPLTDLRI PSVQINFKDLKNIKIPSRFSTPEFTIL NTFHIPSFTIDFVEMKVKIIRTIDQML NSELQWPVPDIYLRDLKVEDIPLARI TLPDFRLPEIAIPEFIIPTLNLNDFQVP DLHIPEFQLPHISHTIEVPTFGKLYSI LKIQSPLFTLDANADIGNGTTSANE AGIAASITAKGESKLEVLNFDFQAN AQLSNPKINPLALKESVKFSSKYLR TEHGSEMLFFGNAIEGKSNTVASLH TEKNTLELSNGVIVKINNQLTLDSN TKYFHKLNIPKLDFSSQADLRNEIKT LLKAGHIAWTSSGKGSWKWACPRF SDEGTHESQISFTIEGPLTSFGLSNKI NSKHLRVNQNLVYESGSLNFSKLEI QSQVDSQHVGHSVLTAKGMALFGE GKAEFTGRHDAHLNGKVIGTLKNS LFFSAQPFEITASTNNEGNLKVRFPL RLTGKIDFLNNYALFLSPSAQQASW QVSARFNQYKYNQNFSAGNNENIM EAHVGINGEANLDFLNIPLTIPEMRL PYTIITTPPLKDFSLWEKTGLKEFLK TTKQSFDLSVKAQYKKNKHRHSIT NPLAVLCEFISQSIKSFDRHFEKNRN NALDFVTKSYNETKIKFDKYKAEKS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HDELPRTFQIPGYTVPVVNVEVSPF TIEMSAFGYVFPKAVSMPSFSILGSD VRVPSYTLILPSLELPVLHVPRNLKL SLPDFKELCTISHIFIPAMGNITYDFS FKSSVITLNTNAELFNQSDIVAHLLS SSSSVIDALQYKLEGTTRLTRKRGL KLATALSLSNKFVEGSHNSTVSLTT KNMEVSVATTTKAQIPILRMNFKQE LNGNTKSKPTVSSSMEFKYDFNSSM LYSTAKGAVDHKLSLESLTSYFSIES STKGDVKGSVLSREYSGTIASEANT YLNSKSTRSSVKLQGTSKIDDIWNL EVKENFAGEATLQRIYSLWEHSTKN HLQLEGLFFTNGEHTSKATLELSPW QMSALVQVHASQPSSFHDFPDLGQ EVALNANTKNQKIRWKNEVRIHSG SFQSQVELSNDQEKAHLDIAGSLEG HLRFLKNIILPVYDKSLWDFLKLDV TTSIGRRQHLRVSTAFVYTKNPNGY SFSIPVKVLADKFIIPGLKLNDLNSV LVMPTFHVPFTDLQVPSCKLDFREI QIYKKLRTSSFALNLPTLPEVKFPEV DVLTKYSQPEDSLIPFFEITVPESQLT VSQFTLPKSVSDGIAALDLNAVANK IADFELPTIIVPEQTIEIPSIKFSVPAGI AIPSFQALTARFEVDSPVYNATWSA SLKNKADYVETVLDSTCSSTVQFLE YELNVLGTHKIEDGTLASKTKGTFA HRDFSAEYEEDGKYEGLQEWEGKA HLNIKSPAFTDLHLRYQKDKKGIST SAASPAVGTVGMDMDEDDDFSKW NFYYSPQSSPDKKLTIFKTELRVRES DEETQIKVNWEEEAASGLLTSLKDN VPKATGVLYDYVNKYHWEHTGLT LREVSSKLRRNLQDHAEWVYQGAI REIDDIDERFQKGASGTTGTYQEWK DKAQNLYQELLTQEGQASFQGLKD NVFDGLVRVTQEFHMKVKHLIDSLI DFLNFPRFQFPGKPGIYTREELCTMF IREVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMYREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFG\PSGVGWTVK YYEGEEKIVSLIKNLLVALKDFHSE YIVSASNF\TSQLSSQVEQFLHRNIQ EYLSILTDPDGKGKEKIAELSATAQ EIIKSQAI\ATKKIISDYHQQFRYKLQ DFSDQLSDYYEK\FIAESKRLI\DLSI QN\YHTFLDYTSREFNWKKLAIQPQ SLNPYMKLAPGELYYHPLIFLKEIFN LFFFSNLNFSHRHRKNCKLPILIKPY SEPALQ
5168	10665	A	5480	2	316	
5169	10666	A	5481	2	401	
5170	10667	A	5482	126	415	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5171	10668	A	5483	3	499	
5172	10669	A	5484	1	241	
5173	10670	A	5485	12	308	
5174	10671	B	5486	394	565	MSAEERLRSSGVLSQKVIAHSLGFD KHGNRLGRGKGYYDAYLKRCLQH QEVKPYTLALAFKEQICLQVPVNEN DMK*
5175	10672	B	5487	674	807	MSAEERLRSSGVLSQKVIAHSEYQK SKRISIFLSMQDEIETEEIIKDIFQRGK ICFLPSVRVPEQSHGYGLGFDKHGN RLGRGKGYYDAYLKRCLQHQEVK PYTLALAFKEQICLQVPVNENDIK*
5176	10673	A	5488	113	339	
5177	10674	A	5490	2	388	FLFFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA
5178	10675	C	5491	197	415	MLLYVGLEPHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASAF*
5179	10676	A	5492	768	1081	KGVLFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5180	10677	A	5494	305	477	
5181	10678	A	5495	1	903	
5182	10679	A	5496	111	295	KPATSVPVIVCVCSSAKPELPLCPAT YTEHHAGQPHWWYHAAR/DLVSW K*QISQRGEINPH
5183	10680	A	5497	1	505	
5184	10681	A	5498	3	345	
5185	10682	A	5499	1	1416	
5186	10683	A	5500	618	707	
5187	10684	C	5501	1729	2511	MDIASTNTSNKSDTNMEQVPATND TIKRLESKLLKNQAKQQSESGRLSL GASRGSSVESLPPTSEGKRMSADMS EIEARIAATTGNGQPRRRSIQDLTVT GTEPGQVSSRSSSPSVRMITTSGPTS EKPTRSHPWTPDDSTDTNGSDNSIP MAYLTLDHQLQPLAPCPNSKESMA VFEQHCKMAQEYMKVQTEIALLLQ RKQELVAELDQDEKDQQNTSRLVQ EHKKLLDENKSLSTYYQQCKKQLE VIRSQQQKRQGTS*
5188	10685	A	5502	1	3489	
5189	10686	A	5503	1	246	
5190	10687	A	5504	40	.124	NVPQFTAKAPCKHEKCLNTNSPDLF EAC*DNIDQTAVSLTAPKTGKRK*R NKVQLS**PQFTAKAPCKHEKCLNT NSPDLFEAC
5191	10688	A	5505	156	1001	GIQQFGQYCLNMLQINQLLSKIKLA NPKEKTAMYLVNELARFNRVQPQY KLLD*RGPAHSKMFSVQLSLGEQT WESEGSSIKKAQQAVGNKALTESTL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PKPI*KPPKSNVNNNPGCITPTVELN GLAMKRGRACHPQAIRSKAIPK**S *LQLSSHV*SEVS\FPIPKIFYVQLTV GNNEFFGEGKTRQAARHNAAMKA LQALQNEPI/LRKISSGMVNQERIW MMTK/HANKSEISLVFEIALKRNMP VSFEVIKESGPPHMKSFVTRVSVGE FSAEGEGNSKK
5192	10689	A	5506	175	411	
5193	10690	A	5507	198	381	
5194	10691	A	5508	137	346	
5195	10692	A	5510	3	136	
5196	10693	A	5511	2	673	
5197	10694	A	5512	1	257	
5198	10695	A	5513	1	712	PRKT/PPAPH\DGDRKELPRTKLLPP API\STD*SQHADRGTEP/GPIRPSIEP GPPVQFGTSDKDSDLRLVVGDSLIA EKELPASVTEAIPVSRDWQLLGSGA ASAEPQSKNLDSGHCVPEHSSSGQR LYPEVFYGSAGPSSSQISGGAMDF\H LAFGSGQGRHLEKGPPDGQRSLGPE GTRSLGCPHPAEGVPLAPYPRGLYI DYKY/MKGERGGRGGVLGLGPHFP SSPFPWSPVPGAVC
5199	10696	A	5514	2	322	
5200	10697	A	5515	1	6470	MSDRSGPTAKGKDGKKYSSLNLFD TYKGKSLEIQKPA\VAPRHGLQSLG KVAIARR/MRPPANLPSLKAENKGN DPNVSLVPKDGTGWASKQEQSDPK SSDASTAQPPESQPLPASQTPASNQP KRPPAAPENTPLVPSGVKSWAQAS VTHGAHGDGGRASSLLSRFSREEFP TLQAAGDQDKAAKERESAEQSSGP GPSLRPQNSTTWRDGGGRGPDELE GPDSKLHHGHDPRGGLQPSGPPQFP PYRGMMPPFMYPPYLPFPPPYGPQG PYRYPTPDGPSRFPRVAGPRGSGPP MRLVEPVGRPSILKEDNLKEFDQLD QENDDGWAGAHEEVDYTEKLKFS DEEDGRDSDEEGAEGHRDSQSASG EERPPEADGKKGNSPNSEPPTPKTA WAETSRPPETEPGPPAPKPPLPPGDY PDRGGPPCKPPAPEDEDEAWRQRR KQSSSEISLAVERARRRREEEERRM QEERRAACAEKLKRLDEKFGAPDK RLKAEPAAPPAAPSTPAPPPAVPKE LPAPPAPPPASAPTPETEPEEPAQAP PAQSTPTPGVAAAPTLVSGGGSTSS TSSGSFEASPVEPQLPSKEGPEPPEE VPPPTTPPVPKVEPKGDGIGPTRQPP SQGLGYPKYQKSLPPRFQRQQQEQ LLKQQQQHQWQQHQQGSAPPTPVP PSPPQPVTLGAVPAPQAPPPPPKALY PGALGRPPPMPPMNFDPRWMMIPP YVDPRLLQGRPPLEFYPPGVHPSGL VPRERSDSLGLSSEPFDRHAPAMLR ERGTPPVDPKLAWVGDVFTATPAE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PRPLTSPLRQAADEDDKGMRSETPP VPPPPPYLASYPGFPENGAPGPPISR FPLEEPGPRPLPWPPGSDEVAKIQTP PPKKEPPKEETAQLTGPEAGRKLPA SRSGAGPPPPRRESRTETRWGPRPG SSRRGIPPEEPGAPPRRAGPIKKPPPP TKVEELPPKPLEQGDETPKPPKPDPL KITKGKLGGPKETPPNGNLSPAPRL RRDYSYERVGPTSCRGRGRGEYFA RGRGFRGTYGGRGRGG/RSEFRSYR EFRGDDGRGGGTGGPNHPPAPRGR HASETRSEGSEYEEIPKRCRQRGSET GSETHESDLAPSDKEAPTPKEGTLT Q/VPLAPPPPGAPP\SP\APARFTC/RG GRRVFTPR/GVPSRRGRGGGR/PPPQ VCPGWSPPAKSLAPKKPPTGPLPPS KEPLKEKLIPGPLSPVARGGSNGGS NVGMEDGERPRRRRHGRAQQQDK PPRFRRLKQERENAARGSEGKPSLT LPASAPGPEEALTTVTVAPAPPRAA AKSPDLSNQNSDQANEEWETASESS DFTSERRGDKEAPPPVLLTPKAVGT PGGGGGGAVPGISAMSRGDLSQRA KDLSKRSFSSQRPGMERQNRRPGPG GKAGSSGSSSGGGGGGPGGRTGPG RGDKRSWPSPKNRSRPPEERPPGLP LPPPPSSSAVFRLDQVIHSNPAGIQ QALAQLSSRQGSVTAPGGHPRHKP GPPQAPQGPSPRPPTRYEPQRVNSG LSSDPHFEEPGPMVRGVGGTPRDSA GVSPFPPKRRERPPRKPELLQEESLP PPHSSGFLGSKPEGPGPQAESRDTG TEALTPHIWNRLHTATSRKSYRPTS MEPWMEPLSPFEDVAGTEMSQSDS GVDLSGDSQVSSGPCSQRSSPDGGL KGAAEGPPKRPGGSSPLNAVPCEGP PGSEPPRRPPPAPHDGDRKELPREQP LPPGPIGTERSQRTDRGTEPGPIRPS HRPGPPVQFGTSDKDSDLRLVVGDS LKAEKELTASVTEAIPVSRDWELLP SAAASAEPQSKNLDSGHCVPEPSSS GQRLYPEVFYGSAGPSSSQISGG\A MDSQLHPNSGG/FRPGTPSLHPYRS QPLYLPPGPAPPSALLSGVALKGQF LDFSTMQATELGKLPAGGVLYPPPS FLYSPAFCPSPLPDTSLLQVRQDLPS PSDFYSTPLQPGGQSGFLPSGAPAQ QMLLPM\VDSQLPVV\NFGSLPPAPP PAPPPLSLLPVGPALQPPSFVVRPQS SPSTGVL\P*LARPFPVYF\GRTELH\P VNIKPFRDF\QKLSSNLGGPGSSRTP P\TGRRPSSLRSFSGLNSRLQSQRLS NLTSGVF\RNQAASTFYQAGLPHPD ALRWIPKPWERTG\RPPR\DGPSRR\ AEEP\GSRGDKEP\GLPPPR
5201	10698	A	5516	2	119	
5202	10699	A	5517	1	325	FFFFF*DRVSLLLPKLECNGTISAHC NLRLPGSSDSPASASSSFFTIHVAPLP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QLRHY*IFYDGTRSLYAG*YSQNLLI YSAPRQPQYHFKDMNKILDSIQRSY TKI
5203	10700	A	5518	228	481	QFFRNTIFF*DRVSLLLPKLECNSAIS AHHNLCLPGSSDSPASASRVAGITG TCHHTRLL\FVFLVETGFYHVSQSG LELLTSGD
5204	10701	A	5519	175	431	LIVKMPFLK*SWKIF*MSK**VMLIH *GFVFLFVC\FF*DRVSLLLPRLECN GPISAHRNLHLPDSSDSPASAYIKGF VRQLSHEE
5205	10702	A	5520	257	453	TKGGGYTQRTAIQFILFIYLFIY*DG VSLLLPRLE*NGAISAHCNLHLPGSS DSQKKTKKNFCTQ
5206	10703	A	5521	277	1230	ISFHLSTFGAPSFFFFFEMEFSLLLPR LECNGAISAHRNLRLPGSSDSPASAS PVGWDYRHVHPRSANFVFFFSRDG VSPCWSGLVSNSRPQMIPPSRPPKV LDTGLATMPGLCLANFCGRNRVSL MCPSWSPELKQSTCLSLPKCWDYR RAAVPGLFILFFLRHRCPTLTQDEV QWCDHSSLQPSTPEIKHPPASASQSS WDQRHAPLHLANFYFYF*FFETES\ HSVT\RLECSGAILAHCNLCLPGSSY SPAPAS*VAGTTGAH/RRLANFFVFL VEMGFHHVRQVDARSLDLVICLPR PPKVLGLQDVSHHRPAYF
5207	10704	A	5522	1	467	FFFLF*EGVSLLLPRLECSGAISA/HC NLHLPGSSDSPASASQEDGITGVRY HAWLIL/VFLVEIGFHHVGQADLKP *PQVIHPPLFFFFLRQSFALVAQAGV QWCDLSSLQTPPPRVQGILLAQPPE YLVAGFTGMRHHTRLFFFFAFLVET GFHPC
5208	10705	A	5523	293	681	QGTILIGLCPFDITPAIVDILLAFWHV R\CPRPTVSCFCKKVVLLV*NFFFFF FFF\ETESCSVTRLECSGVILAHCNL RLPGSSDSHASASRVAETTGVRHHA WPIFVFLVETRFHHVGQAGLELLTS GD
5209	10706	A	5524	274	321	
5210	10707	A	5525	2	733	
5211	10708	A	5527	1	3555	MHYVLNSSSMETFVGEQNYEGSSR LCVCKRTREADDPSARDSVCEGVR ARFNICGINQIVLKCPIWGCENPAQ MGCPPVGKADRCGLLANSATCEKG MFCHADLVGITPTVFPSHPRCKTTA SAKLACQQDVDLDRQSLSSIDKNPS ERGQSQLSNPTDDSWKGRPYANQK LFASLLIKCVVQLELIQTIDNIVFYPA TSKKEDAEHMVAAQQDTLDADIHI ETEDQGMYKYMSSQHLFKLLDCLQ ESHSFSKAFNSNYEQRTVLWRAGF KGKSKPNLLKQETSSLACCLRILFR MYVDENRRDSWEEIQQRLLTVCSE ALAYFITVNSESHREAWTSLLLLLL TKTLKINDEKFKAHASMYYPYLCEI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MQFDLIPELRAVLRKFFLRIGVVYKI WIPEEPSQARCRAILPGFECEAERRQ ERVVPATVRGWGSLLRFCIPTSSYN KCLLNMYCVPDPIAMELSDANLQT LTEYLKKTLDPDPAIRRPAEKFLESV EGNQNYPLLLLTLLEKSQDNVIKVC ASVTFKNYIKRNWRIVEDEPNKICE ADRVAIKANIVHLMLSSPEQIQKQL SDAISIIGREDFPQKWPDLLTEMVN RFQSGDFHVINGVLRTAHSLFKRYR HEFKSNELWTEIKLVLDAFALPLTN LFKICDNAALYAQKYDEEFQRYLPR FVTAIWNLLVTTGQEVKYDLLVSN AIQFLASVCERPHYKNLFEDQNTLT SICEKVIVPNMEFRAADEEAFEDNS EEYIRRDLEGSDIDTRRRAACDLVR GLCKFFEGPVTGIFSGYVNSMLQEY AKNPSVNWKHKDAAIYLVTSLASK AQTQKHGITQANELVNLTEFFVNHI LPDLKSANAIMRSFSLLQEAIIPYIPT LITQLTQKLLAVSKNPSKPHFNHYM FEAICLSIRITCKANPAAVVNFEEAL FLVFTEILQNDV/PSESVDQYRKQIFI LLFQRLQNSKTTKFIKSK*NHLDVL QK**KK\MFGMVLEKIIIPEIQKVSG NVEKKICAVGITKLLTECPPMMDTE YTKLWTPLLQSLIGLFELPEDDTIPD EEHFIDIEDTPGYQTAFSQLAFAGK KEHDPVGQMVNNPKIHLAQSLHKL STACPGRSCGSSPVEDGVCIGAPRSP TASVCFPSLVGSINGPAPAPPPPTVR TTSSGWHCGGACARKARRGPSGRS ALSRLDRSGPS
5212	10709	A	5528	1	4611	
5213	10710	A	5529	58	3051	CQLRSAAGVPSSVSVSPRDPIAMEL SDANLQTLTEYLKKTLDPDPAIRRP AEKFLESVEGNQNYPLLLLTLLEKS QDNVIKVCASVTFKNYIKRN\WRIV EDEPNKICEADRVAIKANIVHLMLS SPEQIQ\KQ\LSDAISI\IGREDFPQ\KW PDL\LTEM\VNRFQSGDFHVINGVLR TAHSLFKRY\RHEFK\SNE\LWTE\IK LVLDAFALP\LTYLF\KATIELCST\H ANDASALRILFSSLILISKLFYSLNFQ DLPEFF\EDNMETWMNNFHTLLTLD NKLLQTDDEEEAGLLELLKSQICDN AALYAQKYDEEFQRYLPRFVTAIW NLLVTTGQEVKYDLLVSNAIQFLAS VCERPHYKNLFEDQNTLTSICEKVI VPNMEFRAADEEAFEDNSEEYIRRD LEGSDIDTRRRAACDLVRGLCKFFE GPVTGIFSGYVNSMLQEYAKNPSV NWKHKDAAIYLVTSLASKAQTQKH GITQANELVNLTEFFVNHILPDLKSA NVNEFPVLKADGIKYIMIFRNQVPK EHLLVSIPLLINHLQAGSIVVHTYAA HALERLFTMRGPNNATLFTAAEIAP FVEILLTNLFKALTLPGSSENEYIMK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AIMRSFSLLQEAIIPYIPTLITQLTQK LLAVSKNPSKPHFNHYMFEAICLSIR ITCKANPAAVVNFEEALFLVFTEILQ NDVQEFIPYVFQVMSLLLETHKNDI PSSYMALFPHLLQPVLWERTGNIPA LVRLLQAFLERGSNTIASAAADKIP GLLGVFQKLIASKANDHQGFYLLNS IIEHMPPESVDQYRKQIFILLFQRLQ NSKTTKFIKSFLVFINLYCIKYGALA LQEIFDGIQPKMFGMVLEKIIIPEIQK VSGNVEKKICAVGITNLLTECPPMM DTEYTKLWTPLLQSLIGLFELPEDD TIPDEEHFIDIEDTPGYQTAFSQLAF AGKKEHDPVGQMVNNPKIHLAQSL HMLSTACPGRVPSMVSTSLNAEAL QYLQGYLQAASVTLL
5214	10711	A	5530	1	396	
5215	10712	A	5531	1	1095	
5216	10713	A	5532	1	1077	
5217	10714	A	5533	1	986	
5218	10715	B	5534	214	975	MEVKTKARELRDECTSLSSRFDQLE ERVLVMENQMNQMKQEEKFREKRI KRNEQSLQEIWDYVKRPNLRVIGVP ESDGENGTKLENTLQDIIQENFPNL ARKANIQIQETQRMPQRYSSRRATP RHIIVRFTKVEMKETMLRAAREKG RVTHKGKPIRLTADLSAETLQAKRE WGPIFNILKEKNFQPRISYPAKLSFIS EGEIKSFTDKQMLRDFVTTRPALKE LLKEALNMERNNQYQHCKNMPNC KDHPG*
5219	10716	A	5535	3	1135	
5220	10717	A	5536	1	1023	
5221	10718	A	5537	2	2747	LHLWGQGTDKQKDSSNLCRLKCPC LTALKRAVVLPARSWRSENGQTAS SKGKLTTRKDIYTENPSVHHHHQRP KVDKTTKMGKKQNRKTGNSKKQS ASPPPKERSASPPPKERSSSPATEQS WREN/DLFDFDELRAEGFKRSNYSE LWEDIQTKGKEVENFEKNLEECITRI TNTEKCLKELMELKTKARELCEEC RSLRSRCDQLEERVSAMEDEVKMN EMNEMKREGKFREKRIKRNEQSLQ EIWDYVKRPNLRLTGVPESDGENG TKLENTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVRFTK VEMKEKILRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFNILKE KNFQPRISCPAKLSFISEGEIKYFTDK QMLRDF\VTTKPALQELLKEALNME RNNRSPSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKEVEN FEKNLEECITRITNTEKCLKELMELK TKARELREECRSLRSRCDQLEERVS AMEDEMNEMKREGKFREKRIKRNE QSLQEIWDYVKRPNLRLIGVPESDV ENGTKLENTLQDIIQENFPNLARQA NVQIQEIQRTPHRFSSRRATTRNLIV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RFTKVEMKEKMLRAAREKGRVTH KGKPIRLTADLLAETLQARREWGPI FNILKEKNFQPRISYPAKLSFISEGEI KYFTEKQMLRDFVTTSPALEELLKE ALNMERNNRTTRQKVNKDIQELNS ALHQADLIDISRTLHPKSTEYTFFSA PHHTYSKIDHIVGSKALLSKCKRTEI ITKCLSDHSAIKLELRIKKLTQNCTT TWKLNNLLLNDYWVQNEMKAEIK MFFENNENKDTTYQNLWDTFKAV CRGKFIALNAHKRKQKRSKTDTLTS QLKELEKEEKHIQKLAEGKK
5222	10719	A	5538	99	432	
5223	10720	A	5539	100	732	
5224	10721	A	5540	242	1300	NPRRSGHSLEAKLRDSSYSELLRDIL QKHEAVHMEALDELYEALAETLM AKESTQGHRSYLLPSGGSVTLSEST AIISHGTTGLVTWDATLYLAEWAIE NPAAFTNRTVLELGSGAGLTGLAIC KDVPPPGIHLQRTCHSRVLEQLRGN VPS\NGLSLEADITAKLDSPRVTVAQ LDWDVATVHQLSAFQPDVVIAADV LYCPEAIMSLVGVLRRLAACREDQ RAPEVYVAFTVRNPETCQLFTTELA PSTCEGVLSLSHLTDKDIRTHRGQA TLELLQTAARPPGSRASTIHPSLPMP RASAPAPPEHSPSWQPCAQMHPQQ PLPAHRDTDNPVPVHVGQPVNYRA NKQAST
5225	10722	A	5541	3	167	
5226	10723	A	5542	2	378	
5227	10724	A	5543	3	359	
5228	10725	A	5544	15	347	
5229	10726	B	5545	141	371	DFGYFYGSSYVAAPDSSRTPGLSRS RDGLLVAKLDLNLCQQVNDVWNF KMTGRYEMYARELAEAVKSNYSPT IVKE*
5230	10727	A	5546	1	1154	MAGAEWKSLEECLEKHLPLPDLQE VKRVLYGKELRKLDLPREAFEAAS REDFELQGYAFEAAEEQLRRPRIVH VGLVQNRIPLPANAPVAEQVSALHR RIKAIVEVAAMCGVNIICFQEAWTM PFAFCTREKLPWTEFAESAEDGPTT RFCQKLAKNHDMVVVSPILERDSE HGDVLWNTAVVISNSGAVLGKTRK NHIPRVGDFNESTYYMEGNLGHPV FQTQFGRIAVNICYGRHHPLNWLM YSINGAEIIFNPSATIGALSESLWPIE ARN\AAIANHCFTCAINRVGTEHFP NEFTSGDGKKAHQDFGYFYGSSYV AAPDSSRTPGLSRSRDGLLVAKLDL NLCQQVNDVWKFKITGRYEMYAR ELAEAVKSNYSPTIVKE
5231	10728	A	5547	424	604	
5232	10729	A	5548	52	318	
5233	10730	A	5549	3	148	
5234	10731	A	5550	258	458	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5235	10732	A	5551	1	217	
5236	10733	A	5552	246	361	
5237	10734	C	5553	69	254	MDHLYNXXXXXXXXXXXXXXXX XXXXXXXXXXEIQFXXXXERERNKN PFPAGDDIISRGVGQ*
5238	10735	A	5554	32	169	NPVPPYPLCPALVFFLLLIYLLIY*PS PLLRMSAPAGKGFLFLSL
5239	10736	A	5555	417	490	
5240	10737	A	5556	2	121	
5241	10738	A	5557	69	398	
5242	10739	A	5558	2	732	GRVPSQCGWIRMRSRSCREDQKPG MDDQRDLISNNEQLSMLGRRPGAP ESKCSRGCPLHSAFSILVTLLLVVQA INAY\FLYH*HGRLDKLTVTPQNLQ LENL\RMKLP\KPPKPVSKMRMATP LL\MQALPMGALPQGPMQNATKYG NMTEDHVMHLLQNADPLKVYPPL KGSFPENLRHLKNTMETIDWKVFES WMHHWLLFEMSRHSLEQKPTDAPP KESLELEDPSSGLGVTKQDLGPVPM
5243	10740	A	5559	2	359	
5244	10741	A	5560	2444	2755	DYYYFFEMESCSVAQAGVQWRDL GSLQPPPP\SSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5245	10742	A	5561	1724	1941	AHLLYEWIFFFFFFEMESHSVAQA GVLWRDLSSLQAPPPG\SQSDSPAS ASWVAGITGACHHARHEWNFKC
5246	10743	A	5562	2	362	
5247	10744	A	5563	138	236	
5248	10745	A	5564	1	278	
5249	10746	A	5565	80	591	RGCKREGLSMSSLIRRVISTAKAPG A\IGPPTVQAVLV\DRTHLHFRDQIG HGPLPSWTSLCPGGVAGRSLNKLL KNMGEIPESLPGCDF\TNVVKTTCSS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLPQKGSRI\EIEA\VAIQ GPLTTAFILSGDPCCVVWDC
5250	10747	A	5566	141	340	
5251	10748	A	5567	209	386	
5252	10749	A	5568	1	346	
5253	10750	A	5569	160	391	
5254	10751	A	5570	101	332	
5255	10752	A	5571	500	752	
5256	10753	A	5572	2	82	
5257	10754	A	5573	3	165	
5258	10755	A	5574	1	219	
5259	10756	A	5575	1	327	
5260	10757	A	5576	2	160	
5261	10758	A	5577	1	189	QQLRHPDLHLQRRSQAQQHQGGQ DS*AQMLCRVPTVPSTTCGRTVSLP LPPKTQGHPHDLPDP
5262	10759	A	5578	2	224	
5263	10760	A	5579	1	1392	
5264	10761	A	5580	1	1272	PGCGRPRAFSLNIADIEEKRGFTSHF VRQTPSPSPNNL*YLIYRRYRQFHA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LQSKLEERFGPDSKSSALACTLPTLP GRRPLPSCCCRAAVRIPALNAYMK VPVGLATLARGRALPPWDPLQGSG CLWSLSTQSQPSVSPDLCAWSLVR* PRQALGARVLDVRIFFYQSPYDSEQ VPQALRRLRPRTRKV*VTSPWAST WPEPAAPRAEVTPAPTLARLSHCNF KAGDVIFLLSRINKDWLEVSSEVRM EVRLKVFVKILKDFPEEDDPTNWLR CYYYEDTISTIKSVAWEGGACPAFL PSLRPLPLTSPSHGSLSHSKAPSGSQ MSHNAVTSHQRPGWPGQPHSPFPH PTLKDLLELTR*GAGNGAGELDTLD AEGDLVRLLSDEDVALMVRQARGL PSQKRLFPWKLHITQKDNYRVYNT MP
5265	10762	A	5581	437	728	
5266	10763	A	5582	570	1648	TQPGTGWARLSTCSLGPSPTMAVA QQLRAESDFEQLPDDVAISANIADIE EKRGFTSHFVFVIEVKTKGGSKYLI YRRYRQFHALQSKLEERFGPDSKSS ALACTLPTLPAKVYVGVKQEIAEM RIPALNAYMKSLLSLPVWVLMDED VRIFFYQSPYDSEQVPQALRRLRPR TRKVKSVSPQGNSVDRMAAPRAEA LFDFTGNSKLELNFKAGDVIFLLSRI NKDWLEGTVRGATGIFPLSFVKILK DFPEEDDPTNWLRCYYYEDTISTIK DIAVEEDLSSTPLLKDLLELTRREFQ REDIALNYRDAEGDLVRLLSDEDV ALMVRQARGLPSQKRLFPWKLHIT QKDNYR\VYNTMP
5267	10764	A	5583	1705	2233	
5268	10765	A	5584	1	354	
5269	10766	A	5585	270	390	
5270	10767	A	5586	3	132	
5271	10768	A	5587	234	362	
5272	10769	A	5588	1	402	
5273	10770	A	5589	2	509	
5274	10771	A	5590	3	1607	SPRPGIPRCFHLVISTEHRRVMTEFG LSWVFLVAIFKGVQCEVQLVESGG DLVQPGGSLRLSCAASGFTFSSYAM HWVRQAPGKGLKYVSGISSNGRRT YYANSVKGRFTISRDNSKNTLYLQ MGSLRAEDMAVYYCARGGDHIVP AAVAPFHMDVWGQGTTVTVSSASP TSPKVFPLSLCSTQPDGNVVIACLPG PGLLPPGATQCDLERKRTGRDRQK LPTQPGCLRGPVHHEQPADPAGHT VPSRQVRDMPREALHESQPGCDCA LPSSLNSTYPISLNSTYPISLMLPPPT VTAPTGPSKDLFLGSKATFTCTLPG L\RDASGVTFTWDALKVGKSAVQG P*RRDLCG\CYSV\SSVLPGCAEAH GTHGEGPSLWHCWPYPESKDPA*PP TLFKIRGNTFPGPRFHLL\PPPSEGAG PWNELVTL\TCLGIGLSAPRMLLVC

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WVAGGHRSLLREKY\LTWA\SRQKP SQGTTTFAVTSILRVAAEDWKKGD TFSCMVGHEALPLAFTQKTIDRLAG KPTHVNVSVVMAEVDGTCY
5275	10772	A	5592	2	315	
5276	10773	A	5593	245	455	
5277	10774	A	5594	1	2863	MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEEESNQATGTSRWDG VSKKAPRHHLSVPCTRPREARQEAE DSTSRLSAESGETDQDAGDVGPDPI PDSYYGLLGTLPCQEALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTIQLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIAK QAERVFPSNVICKTFHSMAYGHIGR KYQSKKKLNLFKLTPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPIWCKNSQGQRVMVEQSE KLNGVLEASRLWDNMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVIKDKFIRRW VHKEGFSGFKRYVTAAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPQLPALR\VEPFS\ EDEW\NLLYVAVTRAKKRLIM\TKS LENILTLAGEYFLQAELTSNVLKTG VVR\CCVG\QCNNAIPVDTVLTMKK L\PITY*ATGK\ENKGGYLCHSCAEQ RIGPLAFLTASPEQVRAMERTVENI VLPRHEALLFLVF
5278	10775	A	5595	3	613	
5279	10776	A	5596	2	1419	PPHLLSSPFVAAPRARATAGAFTLS ASAMQEIAHLQAGQCGNQIGAKFW EVISDEHGIDPTGTYHGDSDLQLERI NVYYNEATG\GNYVPRAVLVDLEP GTMDSVRSGPFGQIFRPDNFVFGQS GAGNNWAKGHYTEGAELVDAVLD VVRKEAESCDCLQGFQLTHSLGGG TGSGMGTLLISKIREEFPDRIMNTFS VVPS\PKCQDTVVEPYNATLSVHQL VENTDETYCIDNEALYDICFRTLKL TTPTYGDLNHLVSATMSGVTTCLRF PGQLNADLRKLAVNMVPFPRLHFF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MPAFAPLTSRGSQQYRGLTVPELTQ QMFDAKNMMAACDPRHGRYLTVA AVFRGRMSMKEVDEQMLSVQSKN SSYFVEWIPNNVKTAVCDIPPRGLK MAVTFIGNSTAIQELFKRISEQFTAM FRRKAFLHWYTGEGMDEMEFTEAE SNMNDLVSEYQQYQDATAEQGEFE EEAEEEVA
5280	10777	A	5603	1	384	
5281	10778	A	5604	185	700	
5282	10779	A	5605	1	414	
5283	10780	A	5606	3	138	
5284	10781	A	5607	1	433	NNPDFKAGV/MALPTL/LQIQRHDD YLVMLKAIRILVQERLTQDAVAKA NQTKEGLPVALDKHILGFDTGDAV LNEAAQILRLLHIEELRELQTKINEA IVAVQAIIHFWHVWKSKCHILGGGS PENWVCSRDLPPLLIAFFFNKV
5285	10782	A	5608	1	459	
5286	10783	A	5609	118	375	VAVVQIIFLPVFIAEKYKDLVPDNSK TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVMLK\A IRILVQERLTQD
5287	10784	A	5610	344	513	
5288	10785	A	5611	3	116	
5289	10786	A	5612	3	869	HEVFSRPRPGEPNREAGTMFRRRLT VLDYHNPAGFNCKDETEFRNFIVW LEDQKIRHYKIEDRG\NLRNIHSSDW PK\FFEKY\LRDVNCPFKIQDRQE\AI DWLLGFAVRPEYG\DNAEKY\KDLV P\DNSK\TADNAPKNAEPWIN\LDVN NPDFK\AGVMALG*PAFRFQRHDD\ FLVNA*RQFRIWVQE\RLT\QDA\VA KAKSNKKRALPVALAQTHILGFD\T GDASSLMKLLEILRIACTYEELRELT DQKSTKAIVAVQAIYC*SQRQDHRL GKSLEDEHFEDLQLSPLL
5290	10787	A	5613	298	403	
5291	10788	A	5614	3	611	
5292	10789	A	5615	192	340	
5293	10790	A	5616	187	361	
5294	10791	A	5617	187	385	
5295	10792	A	5618	2	340	
5296	10793	A	5619	1	702	EKYIQLVRQRALEGALGNTIIYKSQ TAKGTPQETEGTSSGSKSNVRSGKR VPSGRMV/IHSHFPAEVT*E*TRVH WIWQS*CQGESWKQPVPFLCHSGS* RNALL\CLRHDVDALLWQPHSSKQ DDMWEHIATFNALGYVQASKRDK KFFACAPNYSYAALCECLRRVFIYR QPAPMSTVLYNKKGRQA\VGQVAK QQVASLETNDPNLGIQAT\NERLFV LTTKNLFLIKVNTEN
5297	10794	A	5620	3	357	
5298	10795	A	5621	1	1926	
5299	10796	A	5622	1	362	LQTSDEETGFSCLFEYVCAATSFVL VCIINNWSCKAD*DTRWTFRIKIGR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						T/SVVDLLYWRDINITGVVFGATLFL LLSLTVFSIVSVTAYIALALLSVTISF TIYKGVSHAIPKSDEGHPF
5300	10797	A	5623 .	247	533	KSFPGWQTYFSCGWVGCGCLGRGS QNASPPASPLPQLPPG*RRSWPLRG TACRSWSALSGWAAGLYHPPRMPP LMWEAGAGSPGELRGTRIRRER
5301	10798	A	5624	128	667	
5302	10799	A	5625	12	3756	VPRLSRPSPSQSSPTPTTARGSETRP RRRRQQLQHHLHPPAMEDLDQSPL VSSSDSPPRPQPAFKYQFVREPEDEE EEEEEEEDEDEDLEELEVLERKPA AGLSAAPVPTAPAAGAPLMDFGND FVPPAPRGPLPAAPPVAPERQPSWD PSPVSSTVPAPSPLSAAAVSPSKLPE DDEPPARPPPPPPASVSPQAEPVWTP PAPAPAAPPSTPAAPKRRGSSGSVD ETLFALPAASEPVIRSSAENMDLKE QPGNTISAGQEDFPSVLLETAASLPS LSPLSAASFKEHEYLGNLSTVLPTE GTLQENVSEASKEVSEKAKTLLIDR DLTEFSELEYSEMGSSFSVSPKAESA VIVANPREEIIVKNKDEEEKLVSNNI LHNQQELPTALTKLVKEDEVVSSEK AKDSFNEKRVAVEAPMREEYADFK PFERVWEVKDSKEDSDMLAAGGKI ESNLESKVDKKCFADSLEQTNHEK DSESSNDDTSFPSTPEGIKDRSGAYI TCAPFNPAATESIATNIFPLLGDPTSE NKTDEKKIEEKKAQIVTEKNTSTKT SNPFLVAAQDSETDYVTTDNLTKV TEEVVANMPEGLTPDLVQEACESEL NEVTGTKIAYETKMDLVQTSEVMQ ESLYPAAQLCPSFEESEATPSPVLPD IVMEAPLNSAVPSAGASVIQPSSSPL EASSVNYESIKHEPENPPPYEEAMS VSLKKVSGIKEEIKEPENINAALQET EAPYISIACDLIKETKLSAEPAPDFSD YSEMAKVEQPVPDHSELVEDSSPDS EPVDLFSDDSIPDVPQKQDETVMLV KESLTETSFESMIEYENKEKLSALPP EGGKPYLESFKLSLDNTKDTLLPDE VSTLSKKEKIPLQMEELSTAVYSND DLFISKEAQIRETETFSDSSPIEIIDEF PTLISSKTDSFSKLAREYTDLEVSHK SEIANAPDGAGSLPCTELPHDLSLK NIQPKVEEKISFSDDFSKNGSATSKV LLLPPDVSALATQAEIESIVKPKVLV KEAEKKLPSDTEKEDRSPSAIFSAEL SKTSVVDLLY\WRDIKKT\GVVFGA/ SAVFLLLS\LTVF\SIVSVTAYIALAL LSVT\ISF\RIYKGVIQAIQKS\DEGHP FRAISGNL/ESCLYLRELGSGRYSNS\ ALGSMWNCTVKGNFRAPSFFSWM DLVDSL/RSFAVLMWVFTYVGCLG LMVLDTTGFWALNF/ISSSGSWLIYE RHQAQ\IDH\YLGLANKNVKDAMA KIQAKIPG\LKRKAE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5303	10800	A	5626	2	436	RRQFEERQQEMEHVYELLENKMQL LQEESRLAKNEAARMAALVEAEKE CNLELSEKLKGVTKNWEDVPGDQV KPDQ\YTEALAQRDK*VPSVLFL\RL SFAHSQGIQQLSCSLSRT/RQ*ELHY F*DFMGPQPKTFFSGLNFQWYPL
5304	10801	A	5627	3	309	
5305	10802	B	5628	454	645	MTCKKENFSLKLLIYFLEERMQQK YEASREDIYKRNTELKVEVESLKRE LQDKKQPSGLKPWA*
5306	10803	A	5629	1	294	
5307	10804	A	5630	14	228	
5308	10805	A	5631	201	350	
5309	10806	A	5632	262	626	PSARPHCFGLEAMHARSLPCWNCS SRRLLILAFS/WGSE/CCTRKPRIIDV VYNASNNELVRTKTLVKNCIVLIDS TPYR\QWYESH\YALPLGRKKGAKL TPEEEEILNKKRSKKIQKKYDERKE NAKISSLLEEQFQQGKLLACIASRPK QCGRADGYVLEGKELEFYLRK\IKA RKRQINPCFVFTHGNRGVYCFVPTF MLPEYMTVFSAIFPCPAKLIWGGGL QPLALTSASYCPETGSPHC
5310	10807	A	5633	3	452	
5311	10808	A	5634	26	477	NSTDSERTHHGARLLPDKTNVKAA WG\KVGAHAG\EYGAEALERMFLSF PT\TKTYFPHFDL\SHG\SAQVKG/HT GKKVADALTNAVANV\DDMPN\AL SALSDLHAHKLRVDPVNFKLLSHCL AGGPWAAHLPRPSSTPGGATPSLEQ SSWASC
5312	10809	A	5635	1	147	
5313	10810	A	5636	1	503	AAAARAARGTAGPWRSAARLPALP ASSLGAAAMAASAKRKQEEKHLK MLRDMTGLPHNRKCFDCDQRGPTY VNMTVGSFVCTSCSGSLRG*NPPHR VKSISMTTFTQQEIEFLQKHGNEVC P\PEQAKVVASVHASISGSSASSTSS TPEVRPLKSLLGDSAPTLHLN
5314	10811	A	5637	272	360	
5315	10812	A	5638	1	1934	WRRRRRLSRLCRLVWPVSPRTTAP GPRRAQYSQAAAAGSGAGGARRR RAAAAARAARGTAGPRRSAARLPA LPASSLGAAAMAASAKRKQEEKHL KMLRDMTGLPHNRKCFDCDQRGPT YVNMTVGSFVCTSCSGSLRGLNPPH K/VGKSISMTTFTQQEIEFLQKHGNE VCKQIWLGLFDDRSSAIPDFRDPQK VKEFLQEKYEKKRWYVPPEQAKVV ASVHASISGSSASSTSSTPEVKPLKS LLGDSAPTLHLNKGTPSQSPVVGRS QGQQQEKKQFDLLSDLGSDIFAAPA PQSTATANFANFAHFNSHAAQNSA NADFANFDAFGQSSGSSNFGGFPTA SHSPFQPQTTGGSAASVNANFAHFD NFPKSSSADFGTFNTSQSHQTASAV SKVSTNKAGLQTADKYAALANLDN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IFSAGQGGDQGSGFGTTGKAPVGSV VSVPSQSSASSDKYAALAELDSVFS SAATSSNAYTSTSNASSNVFGTVPV VASAQTQPASSSVPAPFGRTPSTNPF VAAAGPSVASSTNPFQTNARGATA ATFGTASMSMPTGFGTPAPYSLPTS FSGSFQQPAFPAQAAFPQQTAFSQQ PNGAGFAAFGQTKPVVTPFGQVAA AGVSSNPFMTGAPTGQFPTGSSSTN PFL
5316	10813	A	5639	1	307	
5317	10814	A	5640	957	3132	GEEEPLWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR *PLGPWCSRR\KKKGAEEEKPKRRR QEKQAACPFYNHEQMGLLRDEALA EVKDMEQLLALGKEARACPYYGSR LAIPAAQLVVLPYQMLLHAATRQA AGIRLQDQVVIIDEAHNLIDTITGMH SVEVSGSQLCQAHSQLLQYVERYG KRLKAKNLMYLKQILYLLEKFVAV LGGNIKQNPNTQSLSQTGTELKTIN DFLFQSQIDNINLFKVCVPSAPQMK HGHCRLNPKLVTQISNSDCPRVQRY CEKSMISRKLFGFTERYGAVFSSRE QPKLAGFQQFLQSLQPRTTEALAAP ADESQASTLRPASPLMHIQGFLAAL TTANQDGRVILSRQGSLSQSTLKFL LLNPAVHFAQVVKECRAVVIAGGT MQPVSDFRQQLLACAGVEAERVVE FSCGHVIPPDNILPLVICSGISNQPLE FTFQKRELPQMMDEVGRILCNLCG VVPGGVVCFFPSYEYLRQVHAHWE KGGLLGRLAARKKIFQEPKSAHQV EQVLLAYSRCIQACGQERGQVTGA LLLSVVGGKMSEGINFSDNLGRCV VMVGMPFPNIRSAELQEKMAYLDQ TLPRAPGQAPPGKALVENLCMKAV NQSIGRAIRHQKDFASVVLLDQRYA RPPVLAKLPAWIRARVEVKATFGPA IAAVQKFLQVYGTSLPLNHLSKLQD TFYPNTSNYAKGR
5318	10815	A	5641	1	1668	
5319	10816	A	5642	947	2782	GEEEPLWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR\ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYYGSRLAIPAAQLV VLPYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSQL CQAHSQLLQYVERYGKRLKAKNL MYLKQILYLLEKFVAVLGGNIKQNP NTQSLSQTGTELKTINDFLFQSQIDN INLFKVQRYCEKSMISRKLFGFTER YGAVFSSREQPKLAGFQQFLQSLQP RTTEALAAPADESQASTLRPASPLM HIQGFLAALTTANQDGRVILSRQGS LSQSTLKFLLLNPAVHFAQVVKECR AVVIAGGTMQPVSDFRQQLLACAG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VEAER\VVEF/SCGHVIPPDNILPLVI CSGISNQPLEFTFQKRELPQMIFQEP KSAHQVEQVLLAYSRCIQACGQER GQVTGALLLSVVGGKMSEGINFSD NLGRCVVMVGMPFPNIRSAELQEK MAYLDQTLPRAPGQAPPGKALVEN LCMKAVNQSIGRAIRHQKDFASVV LLDQRYARPPVLAKLPAWIRARVE VKATFGPAIAAVQKFHREKSASS
5320	10817	A	5643	1143	3233	GEEEPLWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLRGHAEKQAR\ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYYRSRLAIPAAQLV VLSYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGS\Q LCQAHSQLLQYMERYGKRLKAKN LMYLKQILYLLEKFVAVLGGNIKQ NPNTQSLSQTGTELKTINDFLFQSQI DNINLFKVQRYCEKSMISRKLFGFT ERYGAVFSSREQPKLAGFQQFLQSL QPRTTEALAAPADESQASVPQPASP LMHIEGFLAALTTANQDGRVILSRQ GSLSQSTLKFLLLNPAVHFAQVVKE CRAVVIAGGTMQPVSDFRQQLLAC AGVEAERVVEFSCVFGPSLALT\GH VIPPDNILPLVICSGISNQPLEFTFQK RELPQMMDEVGRILCNLCGVVPGG VVCFFPSYEYLRQVHAHWEKGGLL GRLAARKKIFQEPKSAHQVEQVLL AYSRCIQACGQERGQVTGALLLSV VGGKMSEGINFSDNLGRCVVMVG MPFPNIRSAELQEKMAYLDQTLPRA PGQAPPGKALVENLCMKAVNQSIG RAIRHQKDFASIVLLDQRYARPPVL AKLPAWIRARVEVKATFGPAIAAV QKVSPTFFFLRASPPRDHISHCLLSA QFHREKSASS
5321	10818	A	5644	3	744	
5322	10819	A	5645	40	126	
5323	10820	C	5646	187	366	MDERDSHCPYLLSSETTAKGTGLAE SAGKEDPVELDSSLEARVRRRRPST SMPLTSAPC*
5324	10821	A	5647	1	382	TADCAKPVPLAVVSLDSRYGQWES RSSIHA\VTN*ASSSSSSSSSSS\FSR\V YPRFIEFIHFDIQSTGQ/RITSR*HPPR/ DLRDALF*LNSLIPLVRTSSKSAARR RP\GEAPRGTAVPGADPAGGTRPR
5325	10822	A	5648	3	684	QGPRAALGALFPCWAPGKYVHGV RAKHPRATARAPRGSP/LPPHRVSE KTIRVVVFHRRPAGPADPAPGPSRG HRGGAG/EPPTYSTPLMSLHRARLE SSSTGSSFPADSAKPVPLAVVSLDSR *GQWESRSSIHA\VTN*ASSSSSSSSS SS\FSR\VYPRFIEFLHFDIQSTGQ/RIT SRQHPPR/DLRDALF*LNSRIPLVRTS SKSAARRRP\GEAPRGTAAPGADPA GGP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5326	10823	A	5649	2	331	
5327	10824	A	5650	3	340	
5328	10825	A	5651	1	94	
5329	10826	A	5652	2	496	ASMGCSSPLLSLLSLLVGAWLKLG H*TAGHAGGAGKGDGALRPGGREP EAPLPASGMRLQPPAGEVALGAQG ASPPCAFNFLLWNLSIQAQLRRVRG QGCSWRWLVLAQAIEELLGDPALV PTRRQPVGRAAPAPAASSLCCADPA GREVTQVVVVQVVVNSSS
5330	10827	A	5653	3	997	
5331	10828	A	5654	3	131	
5332	10829	A	5655	112	289	
5333	10830	A	5656	35	5228	LDPLGRMVMGIFANCIFCLKVKYLP QQQKKKLQTDIKENGGKFSFSLNPQ CTHIILDNADVLSQYQLNSIQKNHV HIANPDFIWKSIREKRLLDVKNYDP YKPLDITPPPDQKASSSEVKTEGLCP DSATEEEDTVELTEFGMQNVEIPHL PQDFEVAKYNTLEKVGMEGGQEA VVVELQCSRDSRDCPFLISSHFLLDD GMETRRQFAIKKTSEDASEYFENYI EELKKQGFLLREHFTPEATQLASEQ LQALLLEEVMNSSTLSQEVSDLVE MIWAEALGHLEHMLLKPVNRISLN DVSKAEGILLLVKAALKNGETAEQ LQKMMTEFYRLIPHKGTMPKEVNL GLLAKKADLCQLIRDMVNVCETNL SKPNPPSLAKYRALRCKIEHVEQNT EEFLRVRKEVLQNHHSKSPVDVLQI FRVGRVNETTEFLSKLGNVRPLLHG SPVQNIVGILCRGLLLPKVVEDRGV QRTDVGNLGSGIYFSDSLSTSIKYSH PGETDGTRLLLICDVALGKCMDLH EKDFSLTEAPPGYDSVHGVSQTASV TTDFEDDEFVVYKTNQVKMKYIIKF SMPGDQIKDFHPSDHTELEEYRPEF SNFSKVEDYQLPDAKTSSSTKAGLQ DASGNLVPLEDVHIKGRIIDTVAQVI VFQTYTNKSHVPIEAKYIFPLDDKA AVCGFEAFINGKHIVGEIKEKEEAQ QEYLEAVTQGHGAYLMSQDAPDVF TVSVGNLPPKAKVLIKITYITELSILG TVGVFFMPATVAPWQQDKALNEN LQDTVEKICIKEIGTKQSFSLTMSIE MPYVIEFIFSDTHELKQKRTDCKAVI STMEGSSLDSSGFSLHIGLSAAYLPR MWVEKHPEKESEACMLVFQPDLD VDLPDLANESEVIICLDCSSSMEGVT FLQAKEIALHALSLVGEKQKVNIIQF GTGYKELFSYPKHITSNTAAAEFIM SATPTMGNTDFWKTLRYLSLLYPA RGSRNILLVSDGHLQDESLTLQLVK RSRPHTRL\FACGIGSTANRHVLRIL SQCGAGVFEYFNAKSKHSWRKQIE DQMTRLCSPSCHSVSVKWQQLNPD APEALQAPAQVPSLFRNDRLLVYGF IPHCTQATLCALIQEKEFCTMVSTTE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LQKTTGTMIHKLAARALIRDYEDGI LHENETSHEMKKQTLKSLIIKLSKE NSLITQFTSFVAVEKRDENESPFPDI PKVSELIAKEDVDFLPYMSWQGEP QEAVRNQSLLASSEWPELRLSKRK HRKIPFSKRKMELSQPEVSEDFEED ALGVLPAFTSNLERGRVEKLLDLS WTESCKPTATEPLFKKVSPWETSTS SFFPILAPAVGSYLTPTTRAHSPASL SFASYRQVASFGSAAPPRQFDASQF SQGPVPGTCADWIPQSASCPTGPPQ NPPSAPYCGIVFSGSSLSSAQSAPLQ HPGGFTTRPSAGTFPELDSPQLHFSL PTDPDPIRGFGSYHPSAYSPFHFQPS AASLTANLRLPMASALPEALCSQSR TTPVDLCLLEESVGSLEGSRCPVFAF QSSDTESDELSEVLQDSCFLQIKCDT KDDSIPCFLEVKEEDEIVCTQHWQD AVPWTELLSLQTEDGFWKLTPELG LILNLNTNGLHSFLKQKGIQSLGVK GRECLLDLIATMLVLQFIRTRLEKE GIVFKSLMKMDDPSISRNIPWAFEAI KQASEWVRRTEGQYPSICPRLELGN DWDSATKQLLGLQPISTVSPLHRVL HYSQG
5334	10831	A	5657	10	82	
5335	10832	C	5658	189	396	MVHPAGPLASQXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXELWLHHLSSSS *
5336	10833	C	5659	54	485	MXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXRPEDFATYYCQ QNYISPLTFGGGTKVEIXRTVAAPS VFIFPPSX*
5337	10834	A	5660	5	417	
5338	10835	A	5661	3	398	
5339	10836	C	5662	12	451	MXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXFSSYYCQ QSYSVPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQ*
5340	10837	A	5663	3	679	AWWNSETPAQLLFLLLLWLPYTSG EIVLTQAPGTLSLSPGERATLSCRAS QTIGSTYLAWYQQRPGQAPRFLIYG ASSRATGIPDSSSSSSSSSSSSSSSSSS SSSSSSSSSSQQYYTSPLTFGGGTKV EIRRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYA\CEVTHQG
5341	10838	B	5664	94	321	XDRVTITCQATQDIGNYLNWYQHK PGKAPNLLIYDASNLETGVPSRFSG RGSGTHFTFTISSLQPEDIATYYCQQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YX*
5342	10839	A	5665	3	764	AWLESISPTMRVPAQLLGLLLLWIP GSVADIMMTQTPLSLSVSPGQSASIS CKSSQSLLHSDGKTHVYWYLQKPG QSPQLLIYEVSSRFSGVPDRFSGSGS GTDFTLKITRVEAEDVGVYYCQQY NSYLLFTFGPGTKVDIKRTVAA\PSV FIFPP\SDEQLKSG\TASVVCLL\NNFL FP\RRAKVQWEGGINALQSGNSQEC VTE\QDSKGSTYSL\SSTLTVSKADY EKHKVYACEVTHQGLSSPVTKSFN RGEC
5343	10840	A	5666	1	534	RRPRREPWKPQRSFSSSCYS/ELPDT TGEIVLTQSPGTLSLSPGERATLSCR ASQSVSNNYLAWYQQKPGQAPRLL IYDTSSRATGIPDRFSGSASGTDFTL TISRLEPEDFAVYYCQQYGSSPPMY TFGQGTKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKV QW
5344	10841	A	5667	184	621	LHECISVLFPISDTTGEIVLTQSPATL SLSPGERATLSCRASQSVNNNYLA WYQQKPGQPPRLLIYDASNRITGIP ARF\SGSGSGTEFTFHHSAACSLKDF CSLFTVQQLLINWASDSPLGQGTRL GD/IKRTVAAPSVFIFPPSDE
5345	10842	A	5668	156	364	
5346	10843	A	5669	2	2143	SSDGSWWTGFQWREWRQAGRSVN SWDNPKQEVRASSKDKSRGSIQEA MRMQSSAKLLCSAWTLAYSIAVRT LSSDSEGQPPLVIHRQTGSGEDLQQ TPTDLQLRVLTIRRKTNKQKGHPHQ NPISSRRQEITKIRAELKKIETQKPFK KINESRSWFFEKINKIDRLLARLIKK KIEKNQIDAIKNDKGNITTNPTEIQT TIREYYKHLYANKLEHLEEMDKFL DIYTLPRLNQEEVESVNRPITGSEIE AIINSLPTKKSPGPDRFTAELYQRYK EELVPFLLKLFQSIEKEGILPNSFYEA SIILISKPGRDTTKKENFRPISLMNID AKILNKILANQIQQHIKKLIHHHQV GFIPGMQGWFNILKSINVIHHINRTK DKNHMIISIEAEKAFDKIQQPFMLKT LNKLGIDGTYLTYLKIIRAIYDKPTA NIILNGQKLEAFPFKTGTRQGCPLSP LLFNIVLEALARAIRQEKEIKGIQLG KEDVKLSLFADDMIVYLENPIVSAQ NLLKLISNFSEVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVKMAIL PKTLNQKFSYWFRVNKHYIHQRTFP LKETEFNTIATLYNGASP/RTAPKST GTNGHQASGLPRF*RIAFCSALVKS KRKLYQGYLPGQTDRREEGVSWCP GGP
5347	10844	A	5670	1	2781	
5348	10845	A	5671	1	2988	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5349	10846	A	5672	1	3516	
5350	10847	A	5673	1	2850	
5351	10848	A	5674	1	2850	
5352	10849	A	5675	1	3087	
5353	10850	A	5676	1	3111	
5354	10851	A	5677	1	2742	
5355	10852	A	5678	1	3474	
5356	10853	B	5679	1	3264	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALLSKC KRTEIITNCLSDHSAIKLELRIKNLTQ NRSTTWKLNNQLLNDYWAHNEMK AEIKMFFETNENKDTTYQNLWDTF KAVCRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKILQKINESRSWFF ERINKIDRPLARLIKKKREKNQIDAI KNDKGDITTDPTEIQNTIREYYKHL YTNKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGPEIVAIINSLPTKK SPGPDGFTAKFYQRYKEELVPFLLK LFQSIEKEGILPNSFYEASIILIPKPGR DTTKKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGMQGW FNIHKSINVIQHINRPKDKNHMIISID AEKAFDKIQQPFMLKTLNKLGIDGT YFKIISAIYDKPTANIILNGQKVEAFP LKTGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNALITKSI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWNRTEPSEIT PHIYNYLIFDKPEKNKQWGKDSLLN KWCWENWLAICRKLKLDPFLTPYT KINSRWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLKSFCTAKQTTIRVNRQ PTKWEKIFATYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKKHMKKCSSSLAIREMQIK TTMRYHLTPVRMAIIKKSGNNRTW EYNILCSLVPLLCSLLWLHLTDHHL KEDRTKHLTASDNLEKTELSRWKE RALLYEHRVLRPAIDSQHSCAPRRI QGHLVCGSDLTGFMDDVAVILIDVS PF*
5357	10854	A	5680	1	3780	
5358	10855	A	5681	1	3290	MGELITPLSTLDRSTRQKVNKDTQE LNSALHQGDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHILGSKALLSKCKR TEIITNYLSDHSAIKLELRIKNLTQN RSTTWKLNNLLLNDYWIHNEMKAE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IKMFFETNENKDTTYQNLWDAFKA VCRGKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTIKND KGDIATNPTEIQTTIREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQEE VESLNRPITGAEIVAIINSLPTKKSPG PDGFTAESYQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASIILIPKPGRDTT KKENFRLISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQGWFNI RKSINVIQHINRAKDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGIDGTYF KIIRAIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLLFNIVLEVLARAIR QEKEIKGIQSGKEEVKLSLFADDMI VYLENPIVSDQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSW VGRISIVKMAILPKVIYRFSAIPIKLP MTFFTELEKTTLKFIWNQKRARIAK AILSQKNKAGGITLPDFKLYYKATV TKTARYWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKNKQWGKDSLF NKWCWENWLAICRKLKLDPFLTPY TKINSRWIKDLNIRPKTIKTLEENLG STIQDIGMGKDFMSKTPKAMATKD KIDIWDLIKLKSFCTAKETTIRVNGQ PTKWEKIFATYSSDKGLISRICNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKKHMKKCSSSLAIRQMQIK TTMRYHLTP/VKFRSTSHQSP*REAR GPGPLANAGSPGLRQIPETCHLKHP LGMLLLSHHSALSATHNPTPCKLQS SVMFTTSAAMLSDPWGLRKGLGRE MFSCKTTEGNQLEAGAAEQSLYAL PKPSDLQT
5359	10856	A	5682	1	3780	
5360	10857	A	5683	1	2877	
5361	10858	A	5684	1	3126	
5362	10859	A	5685	3	3244	
5363	10860	A	5686	1540	3288	SSGLHPWDARLVQYTQINKCNPAY KQSQRQKPHYYQLEAFPLKTGTRQ QPFMLKT/LYSIVLEVLARAIRQKKE IKGIQLGKEEVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSKVSGYKINV QKSQAFLYTKNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQK NKVGGITLPDFKLYYKATVTKTAW YWYQNRVIDQWNRKEPSEITPHTY NYLIFDKPEKNKQWGKDSLFNKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKTLEENLGITIQD

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IGMGKDFMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRQPTT WEKIFTTYSSDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIIKKSGNNRCWRG CGEIGTLLHCWWDCKLVQPLWKSV WRFLRDLELEIPFDPAIPLLGIYPND YKSCCYKDTCT
5364	10861	A	5687	1182	3406	YQSLAETQPKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQVGFIP GMQGWFNIRKSINVTQHINRAKDK NHMIISIDAEKAFDKIQQPFMLKTLN KLGIDGTYFKIIRAIYDNPTANIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADNMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYTNNR QTESQIMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSG\EGRINIVKMAILP/KELE KTTLKFIWNQKRAHIAKSILNQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEITQHIYSYLI FDKPEKNKQWGKDSLFNKWCWEN WLAICRKLKLDPFLTPYTKINSRWI KDLNVRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKDKIDKWDL VKLKSFCTAKETTIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAA KKHMKKCSSSLAIREMQIKTTMRY HLTPVRMAIIKKSGNNRCWRGCGE TGTLLHCWWDCKLAQPLWKSVWR FLRDLELEIPFDPAIPLLGIYPNDYKS CCYKDTCTRMFIAALFTIAKTWNQP KCPTIIDWIKKMWHIYTMEYYAAIK NDEFVSFVGTWMKLEIIILSKLSQEQ KTTHRIFSLIGGN
5365	10862	A	5688	1	7578	
5366	10863	A	5689	16775	19999	KMIKGISPPIPQKYKTTIREYYKHLY ANKLENLEEMDKFLDTYTLPRLNQ EEVESLNRSITGSEIEAIINSLPTKKSP GPDGFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYESSSILIPKPGRDT TKKENFRPISPISLMNIDAKILNKILA KRIQQHIKKLMHHDQVGFIPGMQG WFNIRKSINVIQHINRAKDKNHMIIS IDAEKAFDKIQQPFMLKTLNKLGID GTYFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVKLSLFA DDMIVYVENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINTVKMAILPKVIYRF NAIPIKLPMPFFTELEKTTLKFIWNQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KRARIAKSILRQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFHKPEKNKQ WGKDSLFNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNVRPKTI KTLEENLGITIQDIGMGKDFMSKTP KAMATKDKIDKWDLIKLKSFCTAK ETTITVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYK\KKTNNPIKKWA RDMNRHFSKEDIYAAKKHMKKCSS SLAIREMQIKTTMRYHLTPVRMAII KKSGNNRSWYFEKINKIDRLLARLI KKKREKNQIDAIKNDKGDITTDPTEI QTTTREYYKHLYANKLENLEEMDK FLDTYNLPRLKQEEVESLNRPIRGSE IVAIINSLPTKKSPGPDGFTAEFYHR YKEELVPLLLKLFQSIEKEVILPNSF YEASIILIPKPDRDTAKKENFRPISLM NIDAKILNKILANRIQQHIKKLIHHD QVGFIPGMQGWFNIRKSVNVIQHIN RTKDKNHMIISIDAEKSFDKIQQHF MLKTLNKLGIDGSYLKIIRATYDKP TANIILNGQKLEAFPLKTGTRHGCP LSPLLFNIVLEVLARAIRQEKEIKGIQ LGKEEVKLSLFIDDMIVYLENPIISA QNLLKLISNFSSLRIQNQCTKITSILV HQ
5367	10864	A	5690	78	308	
5368	10865	A	5691	1	611	GASLGGFLAQKFAEYTHKSPRVHSL ILCNSFSDTSIFNQTWTANSFWLMP AFMLKKIVLGNFSSGPVDPMMADA IDFMVDRLESLGQSELASRLTLNCQ NSYVEPHKIRDIPVTIM\DVFDQSAL STEAKEEMVQA\YPNA\RRAHLKTG GNFPYLCRSAEGN\LMVQIHLLQFH GTKYAAIDPSMVSAEELEVQKGSL GISQEEQ
5369	10866	A	5692	3	301	
5370	10867	A	5693	75	361	
5371	10868	A	5694	3	356	
5372	10869	A	5695	1	583	SPLAAKSPPSLHLLE/AFKNITSSSPE RHIFGEDRVVSEQPQVGTLEERNDV VEALTGSAASRLRGGTSSRRLSSTP LPKAKRSLESEMYLEGLGRSHIASP SPCPDRMPLPSPTESRHSSSIPP\VSSP PEQKVGLYRRQTELQDKSEFSDVD KLAFKDNEEFESSFECVDQKQIEEQ KEEEKIREQQVKERRQR
5373	10870	A	5696	306	4412	RLMMAQSNMFTVADVLSQDELRK KLYQTFKDRGILDTLKTQLRNQLIH ELMHPVLSGELQPRSISVEGSSLLIG ASNSLVADHLQRCGYEYSLSVFFPE SGLAKEKVFTMQDLLQLIKINPTSSL YKSLVSGSDKENQKGFLMHFLKEL AEYHQAKESCNMETQTSSTFNRDS LAEKLQLIDDQFADAYPQRIKFESL EIKLNEYKREIEEQLRAEMCQKLKF FKDTEIAKIKMEAKKKYEKELTMF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QNDFEKACQAKSEALVLREKSTLE RIHKHQEIETKEIYAQRQLLLKDMD LLRGREAELKQRVEAFELNQKLQE EKHKSITEALRRQEQNIKSFEETYDR KLKNELLNFHRLHGVCLALGILI*L WQVLEFGGSSPQECFYFLLEPKGQL VTAGKGK*NCENVPFGIANPDIMLL AVGSQDCA*SLSTKVLTLVGGGQM VQVDWK*PSDYHLGLSLLCAV*I*F TPLLFVSVETN*KVIAFSK*PYDNTT LHFV*LSFGTQFIGSRKGFTGHFMFR GYIPGFSIEDFEVYKLSCLAPSGAPV P*ISSCTDNSLSRKMPEELIFSHSDS\ RYQLELKDDYIIRTNRLIEDERKNK EKAVHLQEELIAINSKKEELNQSVN RVKELELELESVKAQSLAITKQNHM LNEKVKEMSDYSLLKEEKLELLAQ NKLLKQQLEESRNENLRLLNRLAQP APELAVFQKELRKAEKAIVVEHEEF ESCRQALHKQLQDEIEHSAQLKAQI LGYKASVKSLTTQVADLKLQLKQT QTALENEVYCNPKQSVIDRSVNGLI NGNVVPCNGEISGDFLNNPFKQENV LARMVASRITNYPTAWVEGSSPDS DLEFVANTKARVKELQQEAERLEK AFRSYHRRVIKNSAKSPLAAKSPPS LHLLEAFKNITSSSPERHIFGEDRVV SEQPQVGTLKEERNDVVEALTGSE ASRLRGGTSSRRLSSTPLPKAKRS\L ECEMYLEGLGRSHIASPSPCPDRMP LPSPTESRHSLSIPPVSSPPEQKVGLY RRQTELQDKSEFSDVDKLAFKDNE EFESSFEFNSFNYENTLTSKYVAKW LCWELHRILLGKGAPSYFGFSSRAP VSCPHTALPFFVLVLLLRTHGTIVPH AAAGNMPRQLEMGGLSPAGDMSH VDAAAAAVPLSYQHPSVDQKQIEE QKEEEKIREQQVKERRQREERRQSN LQEVLERERRELEKLYQERKMIEES LKIKIKKELEMENELEMSNQEIKDK SAHSENPLEKYMKIIQQEQDQESAD KVPVPWAGQSVGGGHPGLPWLNFL GRESVFSIEDKKSSKKMVQEGSLVD TLQSSDKVERHCIDPLWRTQQQGTI LEAETGPSPDIEPASAFLDLRLPSL
5374	10871	A	5697	3	721	
5375	10872	A	5698	3	265	
5376	10873	A	5699	2	216	
5377	10874	A	5700	3	268	
5378	10875	A	5701	2	465	
5379	10876	A	5702	1	196	
5380	10877	A	5703	2	213	
5381	10878	A	5704	1	438	LQTWGPKQVC/SFFRRGGFEERVLL KNIRENGITGALLPCLDESRFENLGV SSLGERKKLLSYIQRLVQIHVDTMK\ VGYLAGCLVHALGEKQPELQISERD VLCVQIAGLCHDLGHGPFSHMFDG RFIPLARPEVKWTVCIHTVNSQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5382	10879	A	5705	2	1925	
5383	10880	A	5706	330	590	
5384	10881	A	5707	3	139	
5385	10882	A	5708	2	126	
5386	10883	A	5709	1	157	
5387	10884	A	5710	85	489	EKPLRWDSHLSCMLCWQAGFEAEQ KVSGSSRKLAISHALLEMLTPPPAG AMIPPPPSLPGPPRPGMMP\APHMG GPPMMPMMGPPPPGMMPVGPAPG MRPPMGGHMPMMPGPPVTRPPARP MMVPTRPGMTRPDR
5388	10885	A	5711	235	874	VVRRSGFLFCLFVLFLSSMNSASVD GHLSGCRLFLFLSPLFRFYCDYCDT/ YLSPHDSPSVRQTHCSGK\KHIENV KDYYQK\WMEK\QSQSLI\DKTTA\A FQQGKIPPTPFSAPPP\AGA\MIPPPPK /SFPGPPSPLV*MPKHPHMGGPFPW M\PMMGPSFLLGDGWPVG\PASGEL RP\PMG\GHYCQLIAWGPPMDVGPS CPFH*WCPLGPGMTRPDR
5389	10886	A	5712	2	406	FRSPADPPVHCDKE*VLEVQREDED YHDSAKEKDEEDDSITRLLE\FELEA YSLSHNDYDGIKKLLQQLFLKAPVN TAELTNFLIQQNHIGSVIKHTDVS*D SIDDMDEDEAFGFISLLNLPDRKGT QCGEQIQE
5390	10887	A	5713	3	379	AVERGVPHPFDSPVQRDEEEEKEVD TEDDDDDDSDQEKDDEDNALDEEV NIEF\EAYSLSYNDYDGIKKLLPQLFI AAPVNTAKLPDLLIQQNHIGSAIKQ TDVSEDSNDDMDEEEASYSIDRLYN
5391	10888	B	5714	65	188	MWGFRIPADALIQRDEEEEKEVLNE DEDDDDSDKEKDEEDRX*
5392	10889	A	5715	3	365	
5393	10890	A	5716	3	356	
5394	10891	A	5717	1	168	
5395	10892	A	5718	281	422	
5396	10893	A	5719	1	107	
5397	10894	A	5720	3	291	
5398	10895	A	5721	1	1260	WRTAAFWAFTVFLGDIILLTDVVIH EDQWIGETVLQSTFSSQLLNLGSYS SIQPEEYSSVVCEVVLQDLLAYVSS KHSYLRDLPPRQPQRVNSIDFV\EL\ EHLQPDVLVHGSTKELLDFTILTEG S/VYSYRGQKQ\KKVMLTV\DQAQG QHYALVLWGSWGQPGYPQLQRKK GYIWEFKYLFVQCNYTLENLELHTT PWSSCECLFDDDIRAITFKAKFQKS APSFVKISDLATHLEDKCSGVVLIK AQISELAFPITASQKIALNAHSSLKSI FSSLPNIVYTGCAKCGLELETDENRI YKQCFSCLPFTMKKIYYRPALMTAI DGRHDVCIRVESKLIEKILLNISADC LNRVIVPSSEITYGMVVADLFHSLL AVSAEPCVLKIQSLFVLDENSYPLQ QDFSLLDFYPDIVKHGANARL
5399	10896	A	5722	122	390	TFCVRSGLLDFAFPEPWRWGEKWK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NWPESLEVWVLVLAVPLTHCDLGI LCCEDISQVLHVSQQI*PTRPGKR*L LGCAEVVLSSSASPG
5400	10897	A	5723	605	902	
5401	10898	A	5724	116	470	
5402	10899	A	5725	1	9786	
5403	10900	A	5726	10996	13825	MLTLRTRRSDGKMKSGFILGLSRAR SSFPMTKKRATPGHCRDPLEGHLRF LKNIILPVYDKSLWDFLKLDVTTSIG RRQHLRVSTAFVYTKNPNGYSFSIP VKVLADKFITPGLKLNDLNSVLVM PTFHVPFTDLQVPSCKLDFREIQIYK KLRTSSFALNLPTLPEVKFPEVDVLT KYSQPEDSLIPFFEITVPESQLTVSQF T\LPKSVSDGIAALDLNAVANKIADF ELPTIIVPEQTIEIPSIKFSVPAGIVIPS FQALTARFEVDSPVYNATWSASLK NKADYVETSLDSTCSSTVQFLEYEL NVLGTHKIEDGTLASKTKGTLAHR DFSAEYEEDGKFEGLQEWEGKAHL NIKSPAFTDLHLRYQKDKKGISTSA ASPAVGTVGMDMDEDDDFSKWNF YYSPQSSPDKKLTIFKTELRVRESDE ETQIKVNWEEEAASGLLTSLKDNVP KATGVLYDYVNKYHWEHTGLTLR EVSSKLRRNLQNNAEWVYQGAIRQ IDDIDVRFQKAASGTTGTYQEWKD KAQNLYQELLTQEGQASFQGLKDN VFDGLVRVTQKFHMKVKHLIDSLID FLNFPRFQFPGKPGIYTREELCTMFI REVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMYREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFDPSIVGWTVKY YELEEKIVSLIKNLLVALKDFHSEYI VSASNFTSQLSSQVEQFLHRNIQEY LSILTDPDGKGKEKIAELSATAQEII KSQAIATKKIISDYHQQFRYKLQDF SDQLSDYYEKFIAESKRLIDLSIQNY HTFLIYITELLKKLQSTTVMNPYMK LAPGELTIIL
5404	10901	A	5727	3	182	
5405	10902	A	5728	2	221	
5406	10903	A	5729	577	722	
5407	10904	A	5730	3	176	
5408	10905	A	5731	1	496	LLGVAPSRAFQEEILR/DRASFHE/RP NLFALKHPTSKAECTAEKCYRVTK GRGIFPSGSPFKSVTLEDGKTFIPGQ GNNAYVFPGVALGVIAGGIRHIPDEI FLLTAEQIAQEVFEQHLSQGRLYPP LSTIRDVSLRIAIKVLDYAYKHNLDS YTWPKEAMNVQTV
5409	10906	A	5732	228	448	
5410	10907	A	5733	3	1877	EGEDRGLPRTMGAALGTGTRLAPW

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGRACGALPRWTPTAPAQGCHSKP GPARPVPLKKRGYDVTRNPHLNKG MAFTLEERLQLGIHGLIPPCFLSQDV QLLRIMRYYERQQSDLDKYIILMTL QDRNEKLFYRVLTSDVEKFMPIVYT PTVGLACQHYGLTFRRPRGLFITIHD KGHLATMLNSWPEDNIKAVVVTDG ERILGLGDLGCYGMGIPVGKLALYT ACGGVNPQQCLPVLLDVGTNNEEL LRDPLYIGLKHQRVHGKAYDDLLD EFMQAVTDKFGINCLIQFEDFANAN AFRLLNKYRNKYCMFNDDIQGTAS VAVAGILAALRITNNKLSNHVFVFQ GAGEAAMGIAHLLVMALEKEGVPK AEATRKIWMVDSKGLIVKGRSHLN HEKEMFAQD\HPESNSLDEVVRLVK PTAIIGVAAIAEA\FTEQILRNMASF\ RRAPIIFALSNPPRKAECTA\EKCYR VTEGPRGFFASG\SPF*GVLIWEMGK TFIPGGRGNNA\YVFPG\VATG\VIA\ GGIRHIP\DEIFLLDSRAKLPQEVSEQ HL\SQGRLYPPLSTIRDVSLRIAIKVL DYAYKHNLV\SYYPEPKDKEAFCKI PGSYTPDYDSFYT/VDSYIWAQGKA MNVQTV
5411	10908	A	5734	14	304	
5412	10909	A	5735	3	413	
5413	10910	A	5736	2	328	
5414	10911	A	5737	3	472	VTEFAKTCVADESAENCDKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPNLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGERAF KA\VARLSQRFP
5415	10912	A	5738	1	2975	MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLLKCLEQVRKIQGD GAALQEKLCATYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGLFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRHLAQPG GGGDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQQCPFEDHVKLVNEV TEFAKTCVADESA*/ENCDKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPNLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI AR\RHPTCIAP\ELLFFAK\RYKAAFT\ ECCQAADKAACL\LPKLDEL\RDEG KASSAKQRLKCASLQKFGRKSFSK HGAVARL\SQEVFPKLEFCQEVSQV *WTGL*PKFPHGNC\CHGRSCFECC WMDR/RRDLWPKYILWKIQDFDLP S*TGRDCC\EKPLVWGKIPTCICRK WEN*WRLPGLDFAFH*ACLIFVWK VKGCFGQNYCLRAKDVFPGACFLY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						\DYARRAS*FTLFVPAAEDLPRTYET TLEECCAAADPHECYAKVFDEFKPL VEEPQNLIKQNCELFEQLGEYKFQN A\LLVRYT\KKVPQVSTPTLVEVSRN LGKVGSKCCKHPEAKRMPCAEDYL SVVLNHLCVLHEKTPVSDTVTKCC TESFVNTPPCFSALEVDETYVPKHF NAETFTFHAHISTLSQKERQIKKQT ALVDLVKHKPKATKEQLKAVMDD FAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLTPLGPASSLPQSFL LKCLEQVRKIQGDGAALQEKLCAT YKLCHPEELVLLGHSLGIPWAPLSS CPSQALQLAGCLSQLHSGLFLYQGL LQALEGISPELGPTLDTLQLDVADF ATTIWQQMEELGMAPALQPTQGA MPAFASAFQRRAGGVLVASHLQSF LEVSYRVLRHLAQP
5416	10913	A	5739	132	918	
5417	10914	A	5740	59	335	
5418	10915	A	5741	219	642	KGWFLGAFHKL\KTMKHLLLLTMG C/VF*VKSQGVNDN\EEGFFSARGHR P\LDKKREEAP\SLRPAPPPISGRWAI RASSQPKQLATSKGK*ERKSPWIAG KVVFSRLDPDLG\VVCCSLQGCSVC QGGFFLTTRGKGPFQELVV
5419	10916	A	5742	1	359	
5420	10917	A	5743	1	322	
5421	10918	A	5744	2	862	FVDGKLHGRGSTDDKGPVAGWINA LEAYQKTGQEIPVNV\RFCLEGMEE SGSEGLDELIFARKDTFFKDVDYVC ISDNYWLGKKKPCITYGLRGICYFFI EVECSNKDLHSGVYGGSVHEAMTD LILLMEEHKLYDDIDFDIEEFAKDV GAQILLHSHKSHLHLDLLPVVVRLL GQALFHTAHFPDNIPSSSKDILMHR WRYPSLSLHGIEGAFSGSGAKTVIP RKVVGKFSIRLVPNMTPEVVGEQA CGAGTRESMSSLGYPSRAEDDSGLS ALPSQPQPFILYAT
5422	10919	A	5745	455	601	SLAICGSCPFLKTFTITGVFLSSL*YD PSKPALTGRMILSQFVLLNKK
5423	10920	A	5746	25	458	
5424	10921	A	5747	3.	396	
5425	10922	A	5748	2	797	AGPAALGGAGLCRAADAGLCSAGC GFVKVVKNKAYFKRYQVKFRRR\R KGKT\DYYARKR\LVIQDKNKYNTP KYRMIV\RVTNRDIICQIAYA\RIEGD MIVCAA*CTPNLPKYGV\KVGLTNY AAAY\CT\GLLL\ARRL\LNRFG\MDN \IYEGQV\EVTG\DEYNVESIDWSAQ GAF\TCY\LDAGLAR\TT\TGNKVFG\ ALKGMLWMGGLSIPHSSKRFLGLSI PHSTK*ILGYDSENKEFNAEVRRKHI MGQKFADDLHCLIEEDENASKK
5426	10923	A	5749	172	333	
5427	10924	A	5750	2	282	SLSREVQRQMHLVFFSKNKLKAGY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LMSVESSE/CFLEEVG/SQALVAGSY MPPSTVLQQIDS/VANADIINAAKKF VS/GQKSMAAGGNLGHTPLVDEL
5428	10925	A	5751	813	998	
5429	10926	A	5752	1	1418	MKLLTRAGSFSRFYSLKVAPKVKA TAAPAGAPPQPQDLEFTKLPNGLVI ASLENYSPVSRIGLFIKAGSRYEDFS NLGTTHLLRLTSSLTTKGASSFKITR GIEAVGGKLSVTATRENMAYTVEC LRGDVDILMEFLLNVTTAPEFRRWE VADLQPQLKIDKAVAFQNPQTHVIE NLHAAAYQNALANPLYCPDYRIGK VTSEELHYFVQNHFTSARMALIGLG VSHPVLKQVAEQFLNMRGGLGLSG AKANYRGGEIREQNGDSLVHAAFV AESAVAGSAEANAFSVLQHGPRVL GHHVKSGQQQPPAHLHQ\AVAKA\T QQP\FDVSAFNASYSDS\GLFGI\YTIS QGHQLAGDCIK\AA\YNQVKTIA\QG N\LSNTDV\QAAQEPS*KAGIP*WSV ESSE\CF\LEEVRVPRALVAGSY\MPP VHSSFQQI/DSPKRGWGGAKMPDII NGGKRSFVSGPEVQWAASLENLGT LHLFV
5430	10927	A	5753	150	355	
5431	10928	A	5754	2	388	FLFFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA
5432	10929	C	5755	197	415	MLLYVGLEPHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASAF*
5433	10930	A	5756	764	1079	KGVLFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5434	10931	A	5757	213	383	
5435	10932	A	5758	1	981	
5436	10933	A	5759	124	354	
5437	10934	A	5760	2	646	CGGIHGNHTFKMALNQFSDMSFAEI KHKYLWSEPQNCSATKSNYLRGTG PYPPSVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLS LAEQQLVDCAQDFNNHGCQGGLPS QAFEYILYNKGIMGEDTYPY\QGKD GYCK\FQP\GKAIGFVKDV\ANITIYD EEAMVEAVALYNPVSFAFEVTQDF MMYRTGIYSSTSCHKTPDK
5438	10935	A	5761	1	218	
5439	10936	A	5762	272	364	
5440	10937	A	5763	1	1956	
5441	10938	A	5764	105	533	
5442	10939	A	5765	292	568	
5443	10940	A	5766	1	279	

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5444	10941	A	5767	3	352	
5445	10942	A	5768	375	485	TPGLK*FSHLDLLNCWDYRCETVH LAEIAQVSEKQI
5446	10943	A	5769	3	221	
5447	10944	A	5770	793	1039	SFSFTFKMLSGRRETFFFGGRFFWF VV\VFFFFLAGRGSFALVAQAGVQ WRDLRSLQPPPRGFRRFFCLSLPGA CGPRYLGG
5448	10945	C	5771	33	334	MSDSGKSSPVAHSILWIWGRDSDA YRDKQHILWPKRADCTESYPRVPA GGELPTYFLPPENKGLRIHELNSDD YSTEEEAQTPDCSITDFTRRHTLSYL V*
5449	10946	A	5772	194	593	
5450	10947	A	5773	1	877	
5451	10948	A	5774	2	352	
5452	10949	A	5775	3	726	EQEVDYDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCCKHPEA KRMPCAEDYLS\VVLNQLCVLH/EK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCCKHPEA KRMPCAEDYLSRGPEPVMCVA
5453	10950	A	5776	4274	5255	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNIILPKFNHLCTHTHTHTHLTLFST YLKNDRDKTIMCKLSLIG*L\ESLEF GGSGENVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWLDLGT LSV
5454	10951	A	5777	15	218	
5455	10952	A	5778	141	318	
5456	10953	A	5779	1	290	TMSLNRLQEFGTSLVTLDAPHILPE GDELLEENQEGCFS*SFLFATNATL GPRLWSPWLASGLSLPEACASPKH AAQGPHPQKPPRLQPPQHSVCQ

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5457	10954	A	5780	2	643	GTRLFEQLGEYKFQNALLIRYTKKV PQVSTPTLVEVSRNLGKVGSKCCK HPESKKECPVQEDYLSRGSWNQLL CVCIE\KTPVKLTESPKC\CTESLG*T GRPLLFSALGKFDWKHYGFPKRSF NCLKTFHLSMAGFMAHFFEEGRRT NSRKTNWHLFELVETQGPRQQKRQ LKA\VMGGFAAFVEKCCKADDKET CFAEEGKKLVAASQAALGL
5458	10955	A	5781	1	135	
5459	10956	A	5782	1	330	
5460	10957	A	5783	247	434	
5461	10958	A	5784	140	2569	SGSPVLDPSEPQPLAAMHVIKRDGR QERVMFDKITSRIQKLCYGLNMDF VDPAQITMKVIQGLYSGVTTVELDT LAAETAATLTTKHPDYAILAARIA\V SNLHKETKKVFSDV\MEDLYNYINP HNGKHSPMVAKSTL\DIVLANKDRL NSAIIYDRDFSYNYFGFKTLERSYLL KINGKVAERPQHMLMRVSVGIHKE DIDAAIETYNLLSERWFTHASPTLFN AGTNRPQLSSCFLLSMKDDSIEGIY DTLKQCALISKSAGGIGVAVSCIRA TGSYIAGTNGNSNGLVPMLRVYNN TARYVDQGGNKRPGAFAIYLEPWH LDIFEFLDLKKNTGKEEQRARDLFF ALWIPDLFMKRVETNQDWSLMCPN ECPGLDEVWGEEFEKLYASYEKQG RVRKVVKAQQLWYAIIESQTETGTP YMLYKDSCNRKSNQQNLGTIKCSN LCTEIVEYTSKDEVAVCNLASLALN MYVTSEHTYDFKKLAEVTKVVVRN LNKIIDINYYPVPEACLSNKRHRPIGI GVQGLADAFILMRYPFESAEAQLLN KQIFETIYYGALEASCDLAKEQGPY ETYEGSPVSKGILQYDMWNVTPTD LWDWKVLKEKIAKYGIRNSLLIAP MPTASTAQILGNNESIEPYTSNIYTR RVLSGEFQIVNPHLLKDLTERGLWH EEMKNQIIACNGSIQSIPEIPDDLKQL YKTVWEISQKTVLKMAAERGAFID QSQSLNIHIAEPNYGKLTSMHFYGW KQGLKTGMYYLRTRPAANPIQFTL NKEKLKDKEKVSKEEEEKERNTAA MVCSLENRDECLMCGS
5462	10959	A	5785	1	161	
5463	10960	A	5786	2	170	
5464	10961	C	5787	219	398	MSQESVILFYSVGMSLFLFLFRVVT NFTFFPLAVICIRASHLLLACPLPSLS LPHQPTH*
5465	10962	A	5788	2	472	
5466	10963	A	5789	3720	5308	PLLPFLSPPHLTEVEGQGRMVGTEE TWSNCSGAFKPKCSPQPQICLVLAP TRELAQQVQQVADDYGKCSRLKST CIYGGAPKGPQIRDLERGVEICISTP GRLIDFLESGKTNLSRCTYLVLDET DKMLDMGSEPQIL*IGDPIRPDRQTL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MWSATWPKEVRQLAEDFLRDYTQI NVGNLELSANHNILQIVDVCMESEK DHKLIQLMEEIMAEKENKTIIFVETK RRCDDLTRRMRRDGWPAMCIHGD KSQPERDWVLNEFRSGKAPILIATD VASRGLDVEDVKFVINYDYPNSSED YVHRIGRTARSTNKGTAYTFFTPGN LKQARELIKVLEEANQAINPKLMQL VDHRGGGGGGGKGGRSRYRTTSSA NNPNLMYQDECDRRLRGVKDGGR RDSASYRDRSETDRAGYANGSGYG SPNSAFGAQAGQYTYGQGTYGAAA YGTSSYTAQEYGAGTYGASSTTSTG RSSQSSSQQFSGIGRSGQQPQPLMS QQFAQPPGATNMIGYMGQTAYQYP PPPPPPPSRK
5467	10964	A	5790	1	307	
5468	10965	A	5791	2821	5781	
5469	10966	A	5792	1	981	
5470	10967	A	5793	99	1023	NHKDGEKTEQKNGKL*KSECLSKN KAGGITLPDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGNDSLFNKWC WENWLAICRKLKLDPFLTPYTKINS RWIQDLNIRPKNIKTLEEILGNTIQDI GMGKDFKSKTPKAMAIKAKIDKW DLIKLKSFCTEKETTIRVNRQPTEWE KIFAIYSSEKGLISRIYNELQQIYKKK TNNPIQKRVKDMNRHFSKEDIYAA K\KT*KNAHHHMKKCSSSPAIREIQI KTTMRYHLIPIRMVIIKKSGNKGCW RGCGEIGTVLH
5471	10968	A	5794	3	1218	
5472	10969	B	5795	1	1098	MIDKGDIITDPSEIQTTIREYYNYLY TNKLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTTGSEIEAIMNSLPTKK VQDQMDSQPNSTRVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADDMIV YLENPIVSARNLLKLIGNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLKRDVKDLFK ENYKPLLKEIKEDTNKWKSIPCSWV GRINIMKMAILPKVIYRFNAIPNKLP MPFFTELEKTTLKFIWNQKRAHIAK SILSQKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQWNRTEPSEI MPHIYNHLIFDKPDKNKKWGKDSL FNKWCWENWQPYVES*
5473	10970	A	5796	1	1245	
5474	10971	A	5797	1	969	MIVYLENPIVSAQNLLKLIGNFSRVS GYKINVQKSQAFLYTNNRQTENQII SELPFTIASKRIKYLGIQLTRDVKDL FKENYKTLLKEIKEDTKKWKNIPCS WVGRINIVKIAILPKVIYRFSAIPIKL PMTFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRTEPS EIMLHIYKHLIFDKPDKNKQWGKDS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LFNKWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTLEEN LGNTIQDIGTGKDFMSKTPKAMAT KAKIDKWDL/LRFCTAK*TTIRV
5475	10972	B	5798	1	1383	MGDFNTPLSTLDRSKRQKVKKDIQ ELNSALHQVDLIDIYRTPYPKSTEYT FFSAQHHTYSKTDHIVGSKELLSKC KRTEIITNCLSDHSAIKLELRIKKLTQ NRSTTWKLNNLLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLRDTLK AVCRGKFVALNAHQRKQKISKIDTL TSQLKELEKQEQTHSKASRRQEITKI RAELKEIETQKTLQKINDSRSWAIR QEKEIKGIQLGKEEVQLSLFADDMI VHLENPIVSAQNLLKLIGNFSKVSG YKINVKKSQAFLYTNNRQTESQIMS EFPFTIASKRIKYLGIQLTRDVKDLF KENYKTLLNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAISIK LPMTFFTELGKPTLKLVWNQKRVRI AKSILSQKNKAGGIMLPDFKLYYKA TVTKTAWYWYQNRDIDQWNRTEP SEIMPHITTI*
5476	10973	A	5799	1	1272	MIISMDAEKAFDKIQQCFMLKTLNK LGIDGTYLKKIRAIYDKPTVNIILNG QKLEALPLKTGTRQGCPLSPLLFNIV LQALARAIRQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVKAQNLLKL ISNFSKVSGYKISMQKSQAFLYTNN RQIESQIMSELPFTIASKRIKYLGIQL TRDVKDLFKENYKPLLNEIKEDKN KWKNIPCSWVGRINIVKMAILPKFI WRQKRAHIAKSILSQKNKAGGIKLP DFKLYYKATVTKTAWYWYQNRDI DQWNRTEPSEIMLHIHNYLIFDKPD KNKKWRKDSLFNKWCWENWLAK CRKLKLHPFLTPYTKINSRWIKDLH VRPKTIKTLEENLGITIQDKGMGKD FMSKTPEALATKANIDKSDLIKLKS SCK\ETTIRVNRQPTEWEKIFAIYSS
5477	10974	A	5800	1	1398	
5478	10975	A	5801	564	2444	LTNQKKSRTRWIHSRILPEVQGGAV LEVLARAIRQEK\EVKGIQLGKEEV KLSLFADDMIVYLENPIISAQNLLKL IGNFSKVSGYKINVQKSQAFLYTNN RETESQIMSELPFTTASKRIKYLGIQ LTRDVKELFKETYNPLLNEIKEDTT KWKNIPCSWVGRINIVKIAILPKVICI FNAIPIKLPMTFFTELEKTTLKFIRNQ KRARIAKSILSQKNKAGDVTLPDFK LYYKATVTKTVWYWYQNRDIDQW NRTEPSEIILHIYNHLIFDTPDKNKK WGKDSLFNKLCWENWLAICRKLKL DPFFTPYTKINSRWIKDLHVRPKTIK TLEENLGNTIQDIGIGKDFMTKTQK AMATNAEIHKWDLIKLKHFCTAKE TTIRVNRQPTKWENIFAIYSSDKRLI SRIYKELKHIYKRKTNNPINKWAKD

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRMAIIKK SGNNRCWRGCGENHSQQTITRTKIQ TLHVLNHRWELNNENTWTQEGEH HTLGPVVGWGRGEGQQCISPYSMG KASIPHAVLWVFFGLCQNAPNLDW SLVSLWWCLLGFTNFFCKEPDCKY VRLFRPLGIVFATPPLPPPPPSSSTS S
5479	10976	A	5802	1	2430	
5480	10977	A	5803	2022	4573	
5481	10978	A	5804	1169	3077	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQNLLIL QLISNFSKVSGYKINVQKSQAFLYT NNRQTESQMRSELPFTVATKRIKYL GIQLTRDVKDLFKENYKLLLNEIKE DTNKWKNIPRSWVGGRINLVKMAI LPKVIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRALIAKSSLSQKNKTGG ITLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNYLIFDK PDKNKK\WGKDSLFNKWFWENCL AICRKLKLDPFL\TNYTKINSRWIKD LNFRPKTIKTLEDNLGNTIQDIGMG KDFMSLP/KTPEAMATKAKIDKWD LIK\LKSFCTAKETTIRVNRQPTKWE KIFAIYSSDKGLISRIYNELKQIYKK K\TNNPIKKWAKDTNRHFSKEDIYA ANRHMRKCSSSLVIREMQIKTTMR YHLTPVRTAIIKKSGDNRCWRGCGE IGTLLHCWWDCKLVQPLWKSVWR FLRDLELEIPFDPAIPLLGIYPKDYKS CCYKDTCTCMFIAALFTIAKTWNQP KCPTMIDWIKKMWHIYTMEYYAAI KNDEFVSFVGTWMKLEIIILSKLSQE QKTKHCIFSLIGGN
5482	10979	A	5806	133	358	
5483	10980	A	5807	3	164	
5484	10981	A	5808	1573	1720	
5485	10982	A	5809	1573	1720	
5486	10983	A	5810	1	4860	
5487	10984	A	5811	2	2887	VRVIKSEDDVLVVCPTILTEDGMQA QHLGATLALYRLVKGQSVHQLLPP TYRDVWLEWSDAEKKREELNKME TNKPRDLFIAKLLNKLKQQQQQQQ QHSENKRENSEDPEESWENLVSDE DFSALSLESANVEDLEPVRNLFRKL QSTPKYQKLLKERQQLPVFKHRDSI VETLKRHRVVVVAGETGSGKSTQV PHFLLEDLLLNEWEASKCNIVCTQP RRISAVSLANRVCDELGCENGPG\G RNSLCGYQI\RMESRACESTRLLYCT TGVFA*GKLQEDGLSK*CVSMFIVD EV\HER\SVQSDFLLIILKEILQKRSD LHLILMSATVDSEKFSTYFTHCPILR ISGRSYPVEVFHLEDIIEETGFVLEK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DSEYCQKFLEEEEEVTINVTSKAGGI KKYQEYIPVQTGAHADLNPFYQKY SSRTQHAILYMNPHKINLDLILELLA YLDKSPQFRNIEGAVLIFLPGLAHIQ QLYDLLSNDRRFYSERYKVIALHSI LSTQDQAAAFTLPPPGVRKIVLATNI AETGITIPDVVFVIDTGRTKENKYHE SSQMSSLVETFVSKASALQRQGRA GRVRDGFCFRMYTRERFEGFMDYS VPEILRVPLEELCLHIMKCNLGSPED FLSKALDPPQLQVISNAMNLLRKIG ACELNEPKLTPLGQHLAALPVNVKI GKMLIFGAIFGCLDPVATLAAVMTE KSPFTTPIGRKDEADLAKSALAMAD SDHLTIYNAYLGWKKARQEGGYRS EITYCRRNFLNRTSLLTLEDVKQELI KLVKAAGFSSSTTSTSWEGNRASQT LSFQEIALLKAVLVAGLYDNVGKII YTKSVDVTEKLACIVETAQGKAQV HPSSVNRDLQTHGWLLYQEKIRYA RVYLRETTLITPFPVLLFGGDIEVQH RERLLSIDGWIYFQAPVKIAVIFKQL RVLIDSVLRKKLENPKMSLENDKIL QIITELIKTENN
5488	10985	A	5812	1	132	
5489	10986	A	5813	383	667	
5490	10987	A	5814	2444	2755	DYYYFFEMESCSVAQAGVQWRDL GSLQPPPP\SSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5491	10988	A	5815	1724	1941	AHLLYEWIFFFFFFFEMESHSVAQA GVLWRDLSSLQAPPPG\SQSDSPAS ASWVAGITGACHHARHEWNFKC
5492	10989	A	5817	37	2496	
5493	10990	A	5818	2	1814	
5494	10991	A	5819	1	394	
5495	10992	A	5820	2	1785	QLFACVPKTSPPATVISSVTSTCSSL PSVSSAPITSGQAPTTFLPASTSQAQ LSSQKMESFSAVPPTKEKVSTQDQP MANLCTPSSTANSCSSSASNTPGAP ETHPSSSPTPTSSNTQEEAQPSSVSD LSPMSMPFASNSEPAPLTLTSPRMV AADNQDTSNLPQLAVPAPRVSHRM QPRGSFYSMVPNATIHQDPQSIFVT NPVTLTPPQGPPAAVQLSSAVNIMN GSQMHINPANKSLPPTFGPATLFNH FSSLFDSSQVPANQGWGDGPLSSRV ATDASFTVQSAFLGNSVLGHLENM HPDNSKAPGFRPPSQR\VSTSPVGLP SIDPSG\SSPSSSSAPL\ASFSGIPGNQ GFFLQGP\APVGGLLSFNRQHF/SFP HPW\TSASNSCDSPIPSVSSGSSSPLS ATS\APPTLG\QPKGSQCQSRIRKGY LPPIGTERLARILQGGSVAQAPAG\T SFVAPVGHSG\IWSFGVNAVS\EGL\S GWSQSVMG\NHPMAFNNFSGPKAH FSQHQPMERDDSGMVAPSNIFHQP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MASGFVDFSKGLPISMYGGTIIPSHP QLADVPGGPLFNGLHNPDPAWNPM IKVIQNSTECTDAQQVKWA
5496	10993	A	5821	3	125	
5497	10994	A	5822	3448	3831	KNRFCSGVSSNSKSNNSCVYVYIDR DIDTHTYIHIHTNICIHILFFFFFETES HALSPRLECNGVISAHCNLHPPG\SS DSPASAARVAG\ITGTCHHAQLIFFF FVFLVETGFHHAAQAGSQTPDLR*S TPLGFPKC*DYRR/AAIVPGIFLLH*I R*\KVPTLLTDMRNASEYDCDFSTN KIDKEETFS*NASLNLCLLST*PYEM VTHFKGY*ILPLFFFFFLRQSL/SSVT QAGVQWHNLGSLQPLPPGFKQFSC LSLPSSWDYRYQLPRLA/NF/FVFLV ETGFHHAAQAGSQTPDLR

WHAT IS CLAIMED IS:

1.   An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, and complementary sequences thereof.

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2.   An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

10   3.   An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4.   The polynucleotide of claim 1 wherein said polynucleotide is DNA.

15   5.   An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6.   A vector comprising the polynucleotide of claim 1.

20   7.   An expression vector comprising the polynucleotide of claim 1.

8.   A host cell genetically engineered to comprise the polynucleotide of claim 1.

9.   A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
25   associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10.   An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
        (a)   a polypeptide encoded by any one of the polynucleotides of claim 1; and
30   (b)   a polypeptide encoded by a polynucleotide hybridizing under stringent
                        conditions with any one of SEQ ID NO: 1-5497.

11.   A composition comprising the polypeptide of claim 10 and a carrier.

35   12.   An antibody directed against the polypeptide of claim 10.

13.   A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a)   contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

5   b)   detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14.   A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a)   contacting the sample under stringent hybridization conditions with

10   nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b)   amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c)   detecting said product and thereby the polynucleotide of claim 1 in the

15   sample.

15.   The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

20   16.   A method for detecting the polypeptide of claim 10 in a sample, comprising:

a)   contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b)   detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

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17.   A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a)   contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

30   b)   detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18.   A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a)   contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b)   detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19.   A method of producing the polypeptide of claim 10, comprising,

a)   culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-5497, under conditions sufficient to express the polypeptide in said cell; and

b)   isolating the polypeptide from the cell culture or cells of step (a).

20.   An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5498-10994, the mature protein portion thereof, or the active domain thereof.

21   The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22.   A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-5497.

23.   The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24.   The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25.   The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26.   The collection of claim 22, wherein the collection is provided in a computer-readable format.

27.   A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

5   28   A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.